

04-07-00

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PATENT APPLICATION

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## IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Docket No: 28341/6227.1NCP

## PATENT APPLICATION TRANSMITTAL UNDER 37 C.F.R. 1.53

Box Patent Application

Assistant Commissioner for Patents

Washington, D.C. 20231

JCS30 U.S. PRO

09/545199



Sir:

Transmitted herewith for filing is the patent application of

Inventor(s): David E. Lowery, Troy E. Fuller and Michael J. Kennedy

Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

## 1. Type of Application


- ☒ This is a new application for a
- ☒ utility patent.
- ☐ design patent.
- ☐ This is a continuation-in-part application of prior application no.

## 2. Application Papers Enclosed

- 1 Title Page
- 53 Pages of Specification (excluding Claims, Abstract, Drawings & Sequence Listing)
- 8 Page(s) of Claims
- 1 Page(s) of Abstract
- 0 Sheet(s) of Drawings (Figs. \_\_ to \_\_)
- ☐ Formal
- ☐ Informal
- 259 Page(s) of Sequence Listing

## CERTIFICATION UNDER 37 CFR 1.10

I hereby certify that this Patent Application Transmittal and the documents referred to as enclosed therewith are being deposited with the United States Postal Service on **April 6, 2000**, in an envelope addressed to the Assistant Commissioner for Patents, Washington, D.C. 20231 utilizing the "Express Mail Post Office to Addressee" service of the United States Postal Service under Mailing Label No. EM362733684US.

  
Richard Zimmermann



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04/06/00

### 3. Declaration or Oath

- ☐ Enclosed
- ☐ Executed by (check all applicable boxes)
- ☐ Inventor(s)
  - ☐ Legal representative of inventor(s)  
(37 CFR 1.42 or 1.43)
  - ☐ Joint inventor or person showing a proprietary interest on behalf of inventor who refused to sign or cannot be reached
    - ☐ The petition required by 37 CFR 1.47 and the statement required by 37 CFR 1.47 are enclosed. See Item 5D below for fee.
- ☒ Not enclosed - the undersigned attorney or agent is authorized to file this application on behalf of the applicant(s). An executed declaration will follow.

### 4. Additional Papers Enclosed

- ☐ Preliminary Amendment
- ☐ Information Disclosure Statement
- ☐ Declaration of Biological Deposit
- ☒ Computer readable copy of sequence listing containing nucleotide and/or amino acid sequence and statement under 37 C.F.R. §1.821
- ☐ Microfiche computer program
- ☐ Verified statement(s) claiming small entity status under 37 CFR 1.9 and 1.27
- ☐ Associate Power of Attorney
- ☐ Verified translation of a non-English patent application
- ☐ An assignment of the invention
- ☒ Return receipt postcard
- ☐ Other

5. **Priority Applications Under 35 USC 119**

Certified copies of applications from which priority under 35 USC 119 is claimed are listed below

and

- ☐ are attached.  
☐ will follow.

COUNTRY	APPLICATION NO.	FILED

6. **Filing Fee Calculation (37 CFR 1.16)**

A. ☒ **Utility Application**

CLAIMS AS FILED - INCLUDING PRELIMINARY AMENDMENT (IF ANY)						
			SMALL ENTITY		OTHER THAN A SMALL ENTITY	
	NO. FILED	NO. EXTRA	RATE	FEE	RATE	FEE
BASIC FEE				\$345.00		\$690.00
TOTAL	51 - 20	= 31	X 9 =	\$	X 18 =	\$558.00
INDEP.	11 - 3	= 8	X 39 =	\$	X 78 =	\$624.00
<input checked="" type="checkbox"/> First Presentation of Multiple Dependent Claim			+ 130 =	\$	+ 260 =	\$260.00
Filing Fee:				\$	OR	\$2,132.00

B. ☐ **Design Application (\$155.00/\$310.00)** Filing Fee: \$ \_\_\_\_\_

C. ☐ **Plant Application (\$240.00/\$480.00)** Filing Fee: \$ \_\_\_\_\_

D. **Other Fees**

- ☐ Recording Assignment [Fee -- **\$40.00** per assignment] \$ \_\_\_\_\_
- ☐ Petition fee for filing by other than all the inventors or person on behalf of the inventor where inventor refused to sign or cannot be reached [Fee -- **\$130.00**] \$ \_\_\_\_\_
- ☐ Other \$ \_\_\_\_\_

**Total Fees Enclosed      \$2,132.00**

7. Method of Payment of Fees

- ☒ Enclosed check in the amount of: \$2,132.00
- ☐ Charge Deposit Account No. 13-2855 in the amount of: \$ \_\_\_\_\_  
A copy of this Transmittal is enclosed.
- ☐ Not enclosed

8. Deposit Account and Refund Authorization

The Commissioner is hereby authorized to charge any deficiency in the amount enclosed or any additional fees which may be required during the pendency of this application under 37 CFR 1.16 or 37 CFR 1.17 or under other applicable rules (except payment of issue fees), to Deposit Account No. 13-2855. A copy of this Transmittal is enclosed.

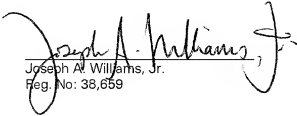
Please refund any overpayment to Marshall, O'Toole, Gerstein, Murray & Borun at the address below.

Please direct all future communications to Joseph A. Williams, Jr., at the address below.

Respectfully submitted,

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April 6, 2000

## JOINT INVENTORS

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Date of Deposit: April 6, 2000

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Richard Zimmermann

## APPLICATION FOR UNITED STATES LETTERS PATENT

# SPECIFICATION

### TO ALL WHOM IT MAY CONCERN:

Be it known that we, David E. Lowery a citizen of the United States of America, residing at 1207 Woodland Drive, Portage, 49024 in the County of Kalamazoo and State of Michigan and Troy E. Fuller a citizen of the United States of America, residing at 111 Dreamfield Drive, Battle Creek, 49014, in the County of Calhoun and State of Michigan and Michael J. Kennedy a citizen of the United States of America, residing at 2364 Quincy Avenue, Portage, 49024, in the County of Kalamazoo and State of Michigan have invented a new and useful ANTI-BACTERIAL VACCINE COMPOSITIONS, of which the following is a specification.

New Patent Application for:

David E. Lowery, Troy E. Fuller, and  
Michael J. Kennedy

For:

ANTI-BACTERIAL VACCINE COMPOSITIONS

Mailing Certification for:

New Patent Application

Attorney Docket No:

28341/6227.1NCP

"EXPRESS MAIL" mailing label No. EM362733684US

Date of Deposit:

April 6, 2000

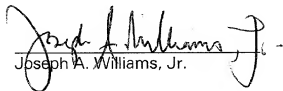
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Richard Zimmermann

**Certificate of 37 C.F.R. §1.821 (f)**

I hereby state that the content of the paper and computer readable copies of the Sequence Listing, submitted in accordance with 37 C.F.R. §1.821(c) and (e), respectively, are the same.



Joseph A. Williams, Jr.

# ANTI-BACTERIAL VACCINE COMPOSITIONS

## FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurella multocida* and *Actinobacillus pleuropneumoniae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

## BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic

bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

*P. multocida* strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as

extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgaris*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet*

Res. 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *P. multocida* and *A. pleuropneumoniae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

## SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H. paraphrohaemolyticus*, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*, *H. somnus*, *Haemophilus minor* group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*, *P. avium* (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. haemolytica*, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P. pneumotropica*, *P. stomatis*, *P.*

volantium (*H. parainfluenzae*), *P. volantium*, *Pasteurella* species A, *Pasteurella* species B, and *Haemophilus paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated *Pasteurella haemolytica*, *Actinobacillus pleuropneumoniae*, *Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella multocida* and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial organisms containing a functional mutation in a gene sequence represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, wherein the mutation inhibits or abolishes expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide encoded by a gene); said functional mutation resulting in attenuated virulence of the bacterial strain. As understood in the art, species homologs include genes found in two or more different species which possess substantial polynucleotide sequence homology and possess the same, or similar, biological functions and/or properties. Preferably polynucleotide sequences which represent species homologs will hybridize under moderately stringent conditions, as described herein by example, and possess the same or similar biological activities and or properties. In another aspect, polynucleotides representing species homologs will share greater than about 60% sequence homology, greater than about 70% sequence homology, greater than about 80% sequence homology, greater than about 90% sequence homology or greater than about 95% sequence homology. Functional mutations that modulate (*i.e.*, increase or decrease) expression and/or biological activity of a gene product include insertions or deletions in the protein coding region of the gene itself or in sequences responsible for, or involved in, control of gene expression. Deletion mutants include those wherein all or part of a specific gene sequence is deleted. In one aspect, the mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene. In another

aspect, the mutation results in an insertion in the gene, wherein the insertion causes decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. Also contemplated are compositions, and preferably vaccine compositions, comprising mutated and attenuated gram negative bacterial organisms, optionally comprising a suitable adjuvant and/or a pharmaceutically acceptable diluent or carrier. In order for a modified strain to be effective in a vaccine formulation, the attenuation must be significant enough to prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1,

3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, as well as related gene sequences from other gram negative  
5 bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122,  
10 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

15 The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit,  
20 and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs,  
25 including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that  
30 include CDR sequences which specifically recognize a polypeptide of the invention. The

invention also provides anti-idiotypic antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

## DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in

virulence by subsequent determination of an approximate LD<sub>50</sub> for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences.

The identification of bacterial, and more particularly *P. multocida* and *A. pleuropneumoniae* virulence genes provides for microorganisms exhibiting reduced virulence (i.e., attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida* and *A. pleuropneumoniae* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida* and *A. pleuropneumoniae* can provide information regarding similar genes, i.e., species homologs, in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *P. haemolytica*,

*Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallinarum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae* and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida* and *A. pleuropneumoniae* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exbB*, *atpG*, and *pnp*

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. In one aspect, therefore, the attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention can bear one or more mutations which result in an insertion in the gene, with the insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is

removed, thereby precluding the possibility that the bacteria will revert to a virulent state. The attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention therefore include those bearing one or more mutation which results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of the virulence gene.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reyrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of

the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida* or *A. pleuropneumoniae* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida* or *A. pleuropneumoniae*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida* or *A. pleuropneumoniae* genome with a marker gene, such as green fluorescent protein (GFP),  $\beta$ -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida* or *A. pleuropneumoniae*. An expression cassette, containing a promoter active in *P. multocida* or *A. pleuropneumoniae* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida* or *A. pleuropneumoniae*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be

immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida* or *A. pleuropneumoniae* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida* or *A. pleuropneumoniae* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida* and *A. pleuropneumoniae* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida*

virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, according to Watson-Crick base pairing rules for DNA. Also preferred are polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. The invention further embraces species, preferably bacterial, homologs of the *P. multocida* and *A. pleuropneumoniae* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a

virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley & Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression control DNA sequence and

a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of *E. coli* or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention. Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cell systems. Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a

protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *Bio/Technology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida* and *A. pleuropneumoniae* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of: a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof; b) DNA molecules encoding *P. multocida* or *A. pleuropneumoniae* polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof; and

c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides, *i.e.*, species homologs and orthologs, that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

Table A  
Conservative Substitutions I

<u>SIDE CHAIN CHARACTERISTIC</u>	<u>AMINO ACID</u>
Aliphatic	G A P I L V
Non-polar	C S T M N Q
Polar - uncharged	D E
Polar - charged	K R
Aromatic	H F W Y
Other	N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant

procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [Biochemistry, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

Table B  
Conservative Substitutions II

	<u>SIDE CHAIN</u> <u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
5	Non-polar (hydrophobic)	
	A. Aliphatic:	A L I V P
	B. Aromatic:	F W
10	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
	A. Hydroxyl:	S T Y
	B. Amides:	N Q
15	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
	Negatively Charged (Acidic):	
	DE	

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies,

humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillitoe, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997). Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent

modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

The identification of *P. multocida* and *A. pleuropneumoniae* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof (*i.e.*, the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical

libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical libraries consist of structural analogs of known compounds or compounds that are identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246

(1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety of proteins, and it is not even necessary to know the identity or function of the second binding protein. The

system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention.

For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (e.g., trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (i.e., mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (e.g., extracted from *Klebsiella pneumoniae*), streptococcal preparations (e.g., OK432), Biostim™ (e.g., 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribi adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (i.e., sterile and non-toxic) liquid, semisolid, or solid diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and

propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, e.g., in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, e.g., by intravenous, intradermal, intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to screening for *P. multocida* mutants. Example 3 addresses methods to determine virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge.

### Example 1

#### Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al.*, *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al.*, *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]<sub>35</sub> sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *KpnI* restriction site in the multiple cloning region and then to introduce a new *KpnI* site in the mini-Tn10 region. The plasmid was digested with *KpnI* and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E. coli* DH5 $\alpha$ : $\lambda$ pir for amplification. *E. coli* DH5 $\alpha$ : ( $\lambda$ pir  $\phi$ 80dlacZ $\Delta$ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r<sub>k</sub><sup>-</sup>, m<sub>k</sub>, supE44, relA1, deoR,  $\Delta$ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *SfiI* which cuts at a unique site within the mini-Tn10 transposable element. A *SfiI*-*KpnI*-*SfiI* adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adaptor was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGCCGCCT SEQ ID NO: 86

TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *Kpn*I site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under conditions including 250  $\mu$ M each dNTP, 1.5 mM Mg(OAc)<sub>2</sub>, 100 pmol each primer TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

TEF14      5'-CATGGTACCCATTCTAAC      SEQ ID NO: 88

TEF15      5'-CTAGGTACCTACAACCTC      SEQ ID NO: 89

TEF26      SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]<sub>35</sub>-  
AAGCTTGGTTAGAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *Kpn*I and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *Kpn*I and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 $\alpha$ : $\lambda$ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100  $\mu$ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems),

200  $\mu$ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM  $MgCl_2$ , 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

5 TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN). Approximately 15 ng of the primary product was labeled in a 50  $\mu$ l PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *Hind*III in a total reaction volume of 90  $\mu$ l and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

Dot blots were prepared using a Hybond<sup>®</sup>-N<sup>+</sup> membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using

approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal vacuum using a Minifold I™ Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150  $\mu$ l of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150  $\mu$ l of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual ).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel purification. Most significantly, PCR was used to generate [NK]<sub>35</sub> sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into *E. coli* S17-1: $\lambda$ pir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96

*E. coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO<sub>2</sub> when grown on plates. Matings were set up by growing each *E. coli* S17-1:λpir /pTEF1:[NK]<sub>35</sub> clone and the TF5 strain to late log phase. Fifty µl of culture for each tagged-pTEF-1 clone was mixed with 200 µl of the TF5 culture and 50 µl of each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates containing 100 mM IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN<sup>50</sup>K<sup>100</sup> plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 µl BHIN<sup>50</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

## Example 2

### Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN<sup>50</sup>K<sup>50</sup>). Plates were incubated without shaking overnight at 37°C in 5% CO<sub>2</sub>. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar)

containing 100  $\mu$ l of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD<sub>540</sub> was monitored using a micro-titer plate reader. At an OD<sub>540</sub> of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100  $\mu$ l from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10<sup>4</sup>, 10<sup>5</sup>, 10<sup>6</sup> CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from 10<sup>-2</sup> to 10<sup>-5</sup> were prepared and plated onto BHIN<sup>50</sup>K<sup>50</sup> plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to prepare genomic DNA according to a previously described protocol [Wilson, In F. M. Ausubel, *et al.*, (ed.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5  $\mu$ g of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

### Example 3

#### Determination of Virulence for *P. multocida* Candidate Mutants

Each potential mutant which exhibited reduced recovery from splenic tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO<sub>2</sub> at 37°C. Approximately six colonies of each mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with 10<sup>2</sup>, 10<sup>3</sup>, 10<sup>4</sup> and 10<sup>5</sup> CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the LD<sub>50</sub> for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate LD<sub>50</sub> of at least 10 fold higher than the wild type strain. The clones and their approximate LD<sub>50</sub> values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to LD<sub>50</sub> values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice (n = 5 to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the LD<sub>50</sub> of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

Table 1  
*P. multocida* Virulence Genes

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	LD <sub>50</sub>
--	wild type	-	0/10	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3 x 10 <sup>6</sup>
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	8.4 x 10 <sup>4</sup>
3	PM1BD7	atpG	5/5, 10/10	10/10	>3 x 10 <sup>5</sup>
74	PM1BE11	yhcJ (H10145)	10/10	5/10	>2 x 10 <sup>5</sup>
70	PM1BF6	yabK (H11020)	3/5, 8/10	9/9	>2 x 10 <sup>5</sup>
19	PM2G8	thaC	4/5, 9/10	9/9	>4 x 10 <sup>5</sup>

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD <sub>50</sub>
76	PM3C9	ymO (HI0146)	3/5		>6 x 105
118	PM3G11	UnkO	4/5, 10/10	10/10	>3 x 105
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB2 (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	>3 x 106
9	PM4G10-T9	dnaA	4/5		>5 x 105
1	PM4D5-T5	atpB	5/5		>4 x 105
53	PM4D5-T1	UnkC2	5/5		>4 x 105
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	>3 x 105
41	PM5F7	mreB	4/5		1 x 103
7	PM5E2	devB	0/5, 3/10	2/3	?
68	PM6H5-T1	xytA	5/5		>3 x 105
78	PM6H8	yggF (HI0719)	5/5, 9/10	9/9	>3 x 105
108	PM7D12	ppp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		~6 x 105
37	PM8C1-T3	mglB	5/5		~6 x 105
58	PM8C1R1-T6	UnkD1	5/5		~6 x 105
45	PM10H7	purF (HI1207)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 105
25	PM10H10-T2	HI1501	5/5		>1 x 104
72	PM11G8-T2	yglK	5/5		>2.4 x 103
21	PM11G8-T4	greA	5/5		>2.4 x 103
84	PM12H6	yyam (HI0687)	3/5, 0/10		~2.2 x 103
33	PM15G8-T2	kdtB	5/5		>1.2 x 105
116	PM15G8-T1	UnkK	5/5		>1.2 x 105
104	PM16G1-T1	hmbR	3/5		>1.9 x 105
29	PM16G1-T2	hxcC	3/5		>1.9 x 105
35	PM16H8	lgtC	5/5, 10/10	10/10	>2.4 x 105
80	PM16H5	vleA (HI0019)	5/5, 10/10		>2.0 x 105
49	PM17H6-T1	sopE	4/5		~6 x 105
120	PM17H6	UnkP	4/5		~6 x 105
5	PM18F5-T8	cap5E	5/5		>2.4 x 105
82	PM18F5-T10	yoiB (HI0345)	5/5		>2.4 x 105
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 105
112	PM19D4	rci	5/5, 8/10	8/8	~1.6 x 105
39	PM20A12	mioC (HI0669)	3/5, 8/10	8/8	~2 x 104
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 106

#### Example 4 Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and

flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

5                    TEF-32            GGCAGAGCATTACGCTGAC            SEQ ID NO: 95  
                   TEF-40    GTACCGCCAGGCGGCCACGCGTATTC    SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for putative interrupted open reading frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison] were used to search for homologous sequences in currently available databases.

15                    In 37% of the clones that were identified as being attenuated, there were multiple insertions of the mini-Tn10 transposable element. Each insertion including its flanking sequence was cloned individually into pGP704 and mated into the wild-type strain to produce new mutants of *P. multocida*, each carrying only one of the multiple original insertions. Individual mutants were retested individually to determine the insertion responsible for the attenuated phenotype. The nucleotide sequence of the disrupted, predicted open reading frame was determined by sequencing both strands, and the predicted amino acid sequence was used to search currently available databases for similar sequences. Sequences either matched known genes, unknown genes, and hypothetical open reading frames previously sequenced or did not match any previously identified sequence. For those genes having homology to previously identified sequences, potential functions were assigned as set out in Table 1.

### Example 5 Identification of Related Genes in Other Species

30                    In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P. multocida*

atpG gene. This result suggested the presence in other bacterial species of homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae* atpG gene as a probe.

*Actinobacillus pleuropneumoniae*, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *EcoRI* and *HindIII* for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N') overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atgG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two

times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *EcoRI* digested DNA. Two bands were detected using *EcoRI* digested DNA from *Pasteurella multocida*.

#### Example 6 Construction of a Library of Tagged-Transposon *P. multocida* Mutants

Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J. Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1: $\lambda$ pir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]<sub>35</sub>) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10  $\mu$ g/ml  $\beta$ -nicotinamide adenine dinucleotide (V<sup>10</sup>), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO<sub>2</sub> when grown on plates. *E. coli* S17-1: $\lambda$ pir ( $\lambda$ pir, *recA*, *thi*, *pro*, *hsdR*( $r_{k^-}$ ,  $m_k^+$ ), RP4-2, (Tc<sup>R</sup>::Mu), (Km<sup>R</sup>::Tn7), [Tnp<sup>R</sup>], [Sm<sup>R</sup>]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100  $\mu$ g/ml ampicillin (Sigma), 50  $\mu$ g/ml nalidixic acid (N<sup>50</sup>)(Sigma), and 50 (K<sup>50</sup>) or 100 (K<sup>100</sup>)  $\mu$ g/ml of kanamycin (Sigma).

Matings were set up by growing each *E. coli* S17-1: $\lambda$ pir/pTEF1:[NK]<sub>35</sub> clone and the AP225 strain to late log phase. A 50  $\mu$ l aliquot of culture for each tagged-pTEF-1 clone was mixed with 150  $\mu$ l of the AP225 culture, and then 50  $\mu$ l of each mating mixture was spotted onto 0.22  $\mu$ M filters previously placed onto BHIV<sup>10</sup> plates containing 100  $\mu$ M IPTG and 10 mM MgSO<sub>4</sub>. Following overnight incubation at 37°C with 5% CO<sub>2</sub>, mating mixtures were washed off of each filter into 2 ml of PBS and 200  $\mu$ l of each was plated onto BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> plates. After selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200  $\mu$ l BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup> making sure that each well in a microtiter plate always contained a

transposon mutant with the same sequence tag. Following overnight growth, 50  $\mu$ l of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

#### Example 7

##### Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20  $\mu$ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180  $\mu$ l of BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup>. Plates were incubated without shaking overnight at 37°C in 5% CO<sub>2</sub>. Overnight plates were then subcultured by transferring 10  $\mu$ l from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100  $\mu$ l of BHIV<sup>10</sup> per well and incubating at 37°C with shaking at 150 rpm. The OD<sub>562</sub> was monitored using a microtiter plate reader. At an OD<sub>562</sub> of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100  $\mu$ l from each of the wells of the microtiter

plate. The culture was diluted appropriately in BHI to approximately  $2 \times 10^6$  CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at  $450 \times g$  for 10 minutes to separate out large debris. Supernatants were then centrifuged at  $2,800 \times g$  to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in dilutions ranging from  $10^{-2}$  to  $10^{-5}$  onto BHIV<sup>10</sup>N<sup>50</sup>K<sup>50</sup> plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In Ausubel, et al.*, (eds.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the  $10^8$  CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also used for inverse PCR reactions and sequencing.

TEF69	GACGTTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTTAAC	SEQ ID NO: 168

The labeled PCR product was then digested with *Hind*III to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG

EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The  $LCPS_{input} / LCPS_{recovered}$  ratio for each mutant was used to determine mutants likely to be attenuated.

Clones selected as being present in the input pool but highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots. A total of 110 clones were selected.

### Example 8 Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haeberli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

Table 2  
*A. pleuropneumoniae* Open Reading Frames

	<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
5	atpH	SEQ ID NO: 134	dksA	SEQ ID NO: 136
	aptG	SEQ ID NO: 132	dnaK	SEQ ID NO: 138
	exbB	SEQ ID NO: 140	HI0379	SEQ ID NO: 144
	OmpP5	SEQ ID NO: 152		
	OmpP5-2	SEQ ID NO: 150	<u>NO Start Codon - NO Stop Codon</u>	
10	tig	SEQ ID NO: 160	pnp	SEQ ID NO: 154
	fkpA	SEQ ID NO: 142	apvA-or 1	SEQ ID NO: 122
	hupA	SEQ ID NO: 146	apvA-or 2	SEQ ID NO: 124
	rpmF	SEQ ID NO: 158	apvB	SEQ ID NO: 126
			apvD	SEQ ID NO: 130
15	<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
	lpdA	SEQ ID NO: 148	tRNA-leu	SEQ ID NO: 162
	potD	SEQ ID NO: 156	tRNA-glu	SEQ ID NO: 163
	yaeE	SEQ ID NO: 164		
	apvC	SEQ ID NO: 128		

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

### Example 9 Competition Challenge of *A. pleuropneumoniae* Mutants with Wild Type APP225

A representative clone from each of the unique attenuated mutant groups identified above that was absent or highly reduced in the recovered population was isolated from the original pool plate and used in a competition challenge experiment with the wild type strain (AP225) to verify the relative attenuation caused by the transposon mutation. Mutant and wild type strains were grown in BHIV<sup>10</sup> to an OD<sub>590</sub> of 0.6 – 0.9. Approximately 5.0 x 10<sup>6</sup> CFU each of the wild type and mutant strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF pig by intratracheal

administration with a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lung lavages were performed as described above. Plate counts were carried out on BHIV<sup>10</sup>N<sup>50</sup> and BHIV<sup>10</sup>N<sup>50</sup>K<sup>100</sup> to determine the relative numbers of wild type to mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the [mutant CFU / wild type CFU]<sub>input</sub> / [mutant CFU / wild type CFU]<sub>recovered</sub>.

Of the 35 potential transposon mutants, 22 were significantly attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that did not seem to be attenuated based on the STM screening results was chosen from one of the pools as a positive control. This mutant had a CI in vivo of approximately 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8. The mutant was subsequently determined to contain an insertion between 2 phenylalanine tRNA's.

Competitive indices for unique attenuated single-insertion mutants are listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated that the mutants were unable to compete effectively with the wild type strains and were therefore attenuated.

**Table 3**  
**Virulence and Proposed Function of *A. pleuropneumoniae* Mutants**

Mutant	Similarity	Putative or Known Functions	C.I.
AP20A6	<i>atpH</i>	ATP synthase	.009
AP7F10	<i>atpG</i>	ATP synthase	.013
AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
AP11E7	<i>exbB</i>	transport of iron compounds	.003,.003,.006
AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
AP13E9	<i>tig</i>	Peptidyl-prolyl isomerase	.050
AP13C2	<i>fkpA</i>	Peptidyl-prolyl isomerase	<.001
AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
AP18F12	<i>hupA</i>	Histone - like protein	.001
AP20F8	<i>dkcA</i>	Dosage dependent suppressor of dnaK mutations	.075
AP5G4	<i>dnaK</i>	Heat shock protein - molecular chaperone	.376

AP17C9	<i>tRNA-leu</i>	Protein Synthesis (gene regulation?)	.059
AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
AP18B2	<i>rpmF</i>	Protein Synthesis	.112
AP10E7	<i>yaeA</i>	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	<i>apvA</i>	Unknown	.157
AP18F5	<i>apvB</i>	Unknown	.103
AP2A6	<i>apvC</i>	Unknown	.091
AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

#### Example 10 Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F<sub>1</sub>- $\gamma$  subunit of the F<sub>0</sub>F<sub>1</sub> H<sup>+</sup>-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F<sub>1</sub>  $\delta$  subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al., Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al., J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase.

While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et al.*, *Mol Microbiol.* 29:1493-507 (1998), Stojiljkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, *et al.*, *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, *et al.*, *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, *et al.*, *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.*

62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duijn, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*, *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J. Bacteriol.* 172:5555-62 (1990), reviewed in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Possible roles

include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J Bacteriol.* 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed

by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A. pleuropneumonia dnaK* mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-*glu* and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21

(1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

### Example 11

#### Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with  $10^{10}$  CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with  $1-5 \times 10^5$  CFU per

pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

**Table 4**  
**Efficacy of *A. pleuropneumoniae* Mutants**

<u>Vaccine</u>	% Mortality following intranasal challenge	
	<u>Vaccination</u>	<u>Challenge</u>
Pleuromune	0	37.5
exbB	0	0
tig	12.5	0
fkpA	12.5	0
HI0385	50.0	0
pnp	0	0
yaeE	0	0
atpG	0	0
None	N/A	50.0

The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of  $10^{10}$  CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest April 6, 2000 CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD<sub>50</sub> using this model was generally  $1 \times 10^7$  CFU, indicating that each of these mutants is at least 100 fold attenuated and that there is a reasonable correlation between CI and attenuation.

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.

5. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

6. The gram-negative bacteria of claim 1 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

7. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124,

126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

9. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

10. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of all or part of said gene.

11. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

12. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

13. The *Pasteurellaceae* bacteria of claim 7 selected from the group consisting of *Pasteurella haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

18. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

19. The attenuated *Pasteurellaceae* bacteria of claim 13 that is a *P. multocida* bacteria.

20. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

21. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

22. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of all or part of said gene.

23. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least

about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

24. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

25. The attenuated *Pasteurellaceae* bacteria of claim 13 that is a *A. pleuropneumoniae* bacteria.

26. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

27. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

28. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of all or part of said gene.

29. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

30. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

31. An immunogenic composition comprising the bacteria according to any one of claims 1 through 30.

32. A vaccine composition comprising the immunogenic composition according to claim 31 and a pharmaceutically acceptable carrier.

33. The vaccine composition according to claim 32 further comprising an adjuvant.

34. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

35. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

36. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112,

114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, .

~~37.~~ A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

38. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 37,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

~~39.~~ A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165.

40. The polynucleotide of claim 39 which is a DNA.

41. A vector comprising the DNA of claim 40.

42. The vector of claim 41 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

43. A host cell stably transformed or transfected with the DNA of claim 40 in a manner allowing the expression of the encoded polypeptide in said host cell.

44. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 43 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

45. A purified polypeptide produced by the method of claim 44.

46. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165.

47. An antibody that is specifically reactive with the polypeptide of claim 46.

48. The antibody of claim 47 that is a monoclonal antibody.

49. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 7, 13, or 19 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

50. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123,

125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165 and identifying an agent that interferes with expression or activity of said gene products.

51. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

# ABSTRACT

Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.

# SEQUENCE LISTING

<110> Lowery E., David  
Fuller E., Troy  
Kennedy J., Michael

<120> Anti-Bacterial Vaccine Compositions

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<151> 1999-09-10

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aacaatagtt ttaaacaata ttcttccatt ttttataagt aagtacttaa atataagca 180
ttttcataaa tatcaataaa ggattagtt atg gca gca gag ctt aca aca gcg 233
                               Met Ala Ala Glu Leu Thr Thr Ala
                               1                               5

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Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala
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cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc 521  
 Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile  
 90 95 100

gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt 569  
 Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly  
 105 110 115 120

att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta 617  
 Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu  
 125 130 135

ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa 665  
 Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys  
 140 145 150

tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt 713  
 Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe  
 155 160 165

aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca 761  
 Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr  
 170 175 180

tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg 809  
 Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met  
 185 190 195 200

tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca 857  
 Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala  
 205 210 215

aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg 905  
 Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp  
 220 225 230

gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg 953  
 Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met  
 235 240 245

atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac 1001  
 Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His  
 250 255 260

taatttttta taaacaaac cagaccttgg gtctaaattt caatcttatg gagaacatta 1061

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 <213> Pasteurella multocida

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 Leu Phe Ser Ile Ile Ser Gly Ala Ile Phe Leu Phe Val Phe Ser Lys  
                   35                                  40                                  45  
 Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe  
                   50                                  55                                  60  
 Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe  
                   65                                  70                                  75                                  80  
 His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys  
                                   85                                  90                                  95  
 Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu  
                                   100                                  105                                  110  
 Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro  
                                   115                                  120                                  125  
 Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe  
                                   130                                  135                                  140  
 Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val  
                                   145                                  150                                  155                                  160  
 Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val  
                                   165                                  170                                  175  
 Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu  
                                   180                                  185                                  190  
 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile  
                                   195                                  200                                  205  
 Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met  
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 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile  
                                   225                                  230                                  235                                  240  
 Thr Leu Gln Ala Phe Ile Phe Met Met Leu Thr Val Val Tyr Leu Ser  
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 acaacaagca ttagtggtat ttgcagtaga gtttggttac ttagaagaag tggacttaga 180  
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 tatgcgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300  
 cattttggat agcttcaaag caaacagtgc gtggtaagtt aacactttaa atggagagac 360  
 aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408  
 Met Ala Gly Ala Lys 5 Glu Ile Arg Thr Lys 10 Ile Ala Ser Val Lys 15  
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 agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456  
 Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys 30  
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 atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504  
 Met Arg Lys Thr Gln Glu Arg Met Ser Ser Arg Pro Tyr Ser Glu 45  
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 aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552  
 Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr 60  
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 aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg gcc atg att 600  
 Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile 75  
 65  
 gtt gtg tcc aca gat cgt ggt ctt tgt ggt gcc tta aac gtg aac ttg 648  
 Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu 95  
 80  
 ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696  
 Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val 110  
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 tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744  
 Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln 125  
 115  
 tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792  
 Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr 140  
 130  
 ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840  
 Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala 155  
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 tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888  
 Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe 175  
 160  
 att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta 936  
 Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu 190  
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 cca gaa tta gat aat gat gaa tta gcc gaa aga aaa caa gtt tgg gat 984  
 Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp 185

tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt 1032  
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val  
210 215 220

cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct 1080  
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala  
225 230 235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128  
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn  
240 245 250 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt 1176  
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg  
260 265 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224  
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala  
275 280 285

gca att taacaaatag aggatcggtta atggcaactg gaaaaattgt acaaatcatc 1280  
Ala Ile

ggtgcggtta ttgacgttga attcccacaa gatgcagttac caaaagtata tgaatgcctta 1340

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tgtatcgcaa tgggatcatc tgaatggatta aaacgcggtt taagcgtaac aaatacgaat 1460

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<211> 289

<212> PRT

<213> Pasteurella multocida

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 35 40 45  
 Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr Lys  
 50 55 60  
 His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val  
 65 70 75 80  
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu Phe  
 85 90 95  
 Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val Ser  
 100 105 110  
 Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln Ser  
 115 120 125  
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 130 135 140  
 Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala Tyr  
 145 150 155 160  
 Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe Ile  
 165 170 175  
 Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu Pro  
 180 185 190  
 Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp Tyr  
 195 200 205  
 Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val Arg  
 210 215 220  
 Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala Ser  
 225 230 235 240  
 Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala  
 245 250 255  
 Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln  
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Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala	
20 25 30	
aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt	144
Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys	
35 40 45	
ctt agc aca gat aaa gcg gtg tac cca att aat gcg atg ggc att tct	192
Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser	
50 55 60	
aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa	240
Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu	
65 70 75 80	
ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca	288
Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala	
85 90 95	
tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc	336
Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly	
100 105 110	
aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca	384
Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr	
115 120 125	
ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa	432
Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln	
130 135 140	
aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc	480
Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr	
145 150 155 160	
ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att	528
Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile	
165 170 175	
tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta	576
Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu	
180 185 190	
agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc	624
Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg	
195 200 205	
atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa	672
Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys	
210 215 220	
ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act	720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr	
225 230 235 240	

gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa 768  
 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu  
 245 250 255

ttc ata cag aaa atg att gag ggt gaa tac atc tca cgg gag gta 813  
 Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val  
 260 265 270

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 ctttatctga ggaacaagat attgagattt tatgttatca ccgtcaatcc tctgagaaaa 933  
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 <213> Pasteurella multocida

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 35 40 45  
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser  
 50 55 60  
 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu  
 65 70 75 80  
 Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala  
 85 90 95  
 Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly  
 100 105 110  
 Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr  
 115 120 125  
 Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln  
 130 135 140

Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr  
 145 150 155 160  
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile  
 165 170 175  
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu  
 180 185 190  
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg  
 195 200 205  
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys  
 210 215 220  
 Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr  
 225 230 235 240  
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 Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser  
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 Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser  
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 Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile  
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Met  
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Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu	
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Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr	
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Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
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Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val	
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Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile	
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Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr				
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Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys				
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Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg				
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Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Ser Leu				
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Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu				
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Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu				
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Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys				
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Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu				
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Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly				
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Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr				
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Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys	
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Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu	
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Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp	
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gat tta gcg ggg agt tca gct aaa ttg tct gtt gaa aga aca cat gag Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu 1270 1275 1280			4376
aca aaa cga acg aca gaa acg ggg gat att gtt act aag att ggt ggc Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly Gly 1285 1290 1295			4424
aat gtc aca ctg tca gca cgc agt ggt agt gtg aac ctt aaa aat gta Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn Val 1300 1305 1310			4472
caa agt gat gaa caa gct aat ttg acc tta aga gca aaa gaa gat gtg Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp Val 1315 1320 1325			4520
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ggc gcc tgt act gcc ggt gtt agc aca tca ctt gaa gga aat gaa agc Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu Ser 1365 1370 1375			4664
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cgc aac atg aaa gtt gaa gca ggt cgc gat ttt aat gtt gtc agt tcg Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser Ser 1395 1400 1405			4760
aat att gat gca gat aag ctc gat ctc cac gtt aaa gga aaa acg aat Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr Asn 1410 1415 1420 1425			4808
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cca acc ggt aat gtt ggt ttc ggt tat acc aat gag acc gaa agc aag Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys 1460 1465 1470			4952

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Gln Thr His Asp Leu Asn Leu Glu Gly Tyr Leu Val Ser Asn Asp	
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Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala Leu	
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His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val Gly	
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Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Arg Ala	
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Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln Phe	
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Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys Asn	
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Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr Thr	
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Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr Ser	

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Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr Thr			
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Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp Pro			
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Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp Gly			
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Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys			
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Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser Pro			
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Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn Lys			
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Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu Arg			
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Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn Lys			
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Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu Phe			
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Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala Ile			
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Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val Val			
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Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala Pro			
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Val Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg  
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Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn  
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Leu Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala  
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 Ser Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys  
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 cgttggagtt tctcagtag ttaccgttta tataaaaatc atcatgctaa ccagcaacgc 600  
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 ggtgtgagtg gtgttacgca acatcgtcaa aaaccgattt attatttctc aggatcactt 1440

tctttttaat ctctttttaag tttaaggatt aacttaat atg aac aaa aat cgt tac 1496  
 Met Asn Lys Asn Arg Tyr  
 1 5

aaa ctc att ttt agt caa gtc aaa ggt tgt ctc gtt cct gtg gca gaa 1544  
 Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu  
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tgt att aac tca gct att agc aat ggt tca tct gat tca aca tcc aca 1592  
 Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr  
 25 30 35

tca gaa caa gtt gaa gag gaa cct ttc ctt cta gaa caa tat tca ctt 1640  
 Ser Glu Gln Val Glu Glu Pro Phe Leu Leu Gln Tyr Ser Leu  
 40 45 50

tcc tcc gtg tct tta tta gta aaa agc acg ttc aat cct gtt tgg tat 1688  
 Ser Ser Val Ser Leu Leu Val Lys Ser Thr Phe Asn Pro Val Ser Tyr  
 55 60 65 70

gca atg caa ttg act tgg aaa cag ctt tct att tta ttt tta act gtg 1736  
 Ala Met Gln Leu Thr Trp Lys Gln Leu Ser Ile Leu Phe Leu Thr Val  
 75 80 85

att tct gtt cct gtt ttg gct gag gga aaa ggg gat gaa aga aat caa 1784  
 Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln  
 90 95 100

tta aca gtg att gat aat agc gat cat att aaa tta gat gca tct aat 1832  
 Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn  
 105 110 115

ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt 1880  
 Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr Gln Ala Glu Asn Lys Val  
 120 125 130

ctg gtt att gat att gct aaa cca aat ggg aaa ggg att tca gat aac 1928  
 Leu Val Ile Asp Ile Ala Lys Pro Asn Gly Lys Gly Ile Ser Asp Asn  
 135 140 145 150

cgt ttt gaa aaa ttt aat att cca aat agc gcg gtg ttt aat aat aat 1976  
 Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser Ala Val Phe Asn Asn Asn  
 155 160 165

ggg act gaa gcg cag gca aga tca aca tta att ggt tac att cgg caa 2024  
 Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu Ile Gly Tyr Ile Pro Gln  
 170 175 180

aat caa aat tta agg gga ggg aaa gaa gct gat gtt ata tta aat caa 2072  
 Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala Asp Val Ile Leu Asn Gln  
 185 190 195

gtg aca ggt cct caa gaa agt aaa att gtt ggc gcg ctt gaa gta tta 2120  
 Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu  
 200 205 210

ggt aaa aaa gct gat atc gtc att gca aac caa aat ggt att acc tta 2168  
 Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu  
 215 220 225 230

aat ggt gta aga aca ata aat tca gat cgt ttt gtt gcc act acg agt 2216

Asn Gly Val Arg Thr	Ile Asn Ser Asp Arg Phe Val Ala Thr Thr Ser	
235	240	245
gag ctt ata gat ccg aat cag atg atg tta aag gtt aca aaa gga aat	2264	
Glu Leu Ile Asp Pro Asn Gln Met Met Leu Lys Val Thr Lys Gly Asn		
250	255	260
gtg atc att gat att gat ggt ttt tct aca gat gga tta aag tat tta	2312	
Val Ile Ile Asp Ile Asp Gly Phe Ser Thr Asp Gly Leu Lys Tyr Leu		
265	270	275
gat att att gct aaa aaa att gaa caa aag caa tca att aca tca ggg	2360	
Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys Gln Ser Ile Thr Ser Gly		
280	285	290
gat aat tca gaa gca aaa aca gat gtc act ctt att gcg ggt tcc agt	2408	
Asp Asn Ser Glu Ala Lys Thr Asp Val Thr Leu Ile Ala Gly Ser Ser		
295	300	305
gaa tat gat tta agc aaa cat gag ctg aaa aaa acg agc ggt gaa aat	2456	
Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn		
315	320	325
gta tct aat gat gtt att gct atc acg gga tct agt aca ggc gca atg	2504	
Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met		
330	335	340
cat ggt aaa aat att aag ttg att gtg aca gat aaa ggt gca ggc gta	2552	
His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val		
345	350	355
aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg	2600	
Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met		
360	365	370
aat gaa ggt gac tta gaa ctt ggc aat acg att cag caa aca gtg gta	2648	
Asn Glu Ala Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val		
375	380	385
aaa aaa gac cga aat att cga gcc aag aaa aaa att gaa gtg aaa aac	2696	
Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys Lys Ile Glu Val Lys Asn		
395	400	405
gct aat cgt gtt ttt gtt ggt agt caa acg aaa tca gat gaa att tct	2744	
Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser		
410	415	420
tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt	2792	
Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser		
425	430	435
acg aca caa gcc aaa atc gta gca aag ggt gcc ctg tct att gag caa	2840	
Thr Thr Gln Ala Lys Ile Val Ala Lys Gly Ala Leu Ser Ile Glu Gln		
440	445	450
aat gcg aag ctc gtc gct aaa aag ata gat gtg gca aca gaa act cta	2888	
Asn Ala Lys Leu Val Ala Lys Lys Ile Asp Val Ala Thr Glu Thr Leu		
455	460	465
act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat	2936	
Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn		
475	480	485

aat ttg att aat gat aaa gaa att tat gct gaa cgg aaa ttg agt att 2984  
Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala Glu Arg Lys Leu Ser Ile  
490 495 500

ttg acg aaa gga aaa gat ctt gaa att att caa gat aga tat ttg tct 3032  
Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile Gln Asp Arg Tyr Leu Ser  
505 510 515

cca ctg atg cgc gta aaa agt agt gtc cgc ttt tta ggc tct ccg ttt 3080  
Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe  
520 525 530

ttc tca ata tct ccg tcg atg ctc gca agc ctt agt gca cag ttt aag 3128  
Phe Ser Ile Ser Pro Ser Met Leu Ala Ser Leu Ser Ala Gln Phe Lys  
535 540 545 550

cct ggt ttt gtg aat aag gga ctc att gaa agt cgc ggg agt gca gaa 3176  
Pro Gly Phe Val Asn Lys Gly Leu Ile Glu Ser Ala Gly Ser Ala Glu  
555 560 565

tta act ttt aaa gaa aaa acc agt ttt tta aca gag ggc aat aat ttt 3224  
Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe  
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att aga gct aaa gat cgc tta ac 3247  
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<212> PRT

<213> Pasteurella multocida

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Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu  
35 40 45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr  
50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser  
65 70 75 80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys  
85 90 95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
100 105 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr  
115 120 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly  
130 135 140

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser  
 145 150 155 160  
 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu  
 165 170 175  
 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala  
 180 185 190  
 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val  
 195 200 205  
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn  
 210 215 220  
 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg  
 225 230 235 240  
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu  
 245 250 255  
 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr  
 260 265 270  
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys  
 275 280 285  
 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr  
 290 295 300  
 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys  
 305 310 315 320  
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly  
 325 330 335  
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr  
 340 345 350  
 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn  
 355 360 365  
 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr  
 370 375 380  
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys  
 385 390 395 400  
 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr  
 405 410 415  
 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys  
 420 425 430  
 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly  
 435 440 445  
 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp  
 450 455 460  
 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu  
 465 470 475 480

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala  
485 490

Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile  
500 505 510

Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg  
515 520 525

Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser  
530 535 540

Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu  
545 550 555 560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu  
565 570 575

Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu  
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<212> DNA  
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Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile  
1 5 10 15

cat gct tac caa aac cag ccc cta tca aca aaa gtt gtt ttt caa tta 96  
His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu  
20 25 30

gtg aaa gat ttg acg gaa gtt tta tac cgt tct ggc tac gtg aca agt 144  
Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser  
35 40 45

gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt 192  
Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe  
50 55 60

att gta ctg tgg gga aga act cgc gat ctg ttt gtg aat ggg gag aaa 240  
Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys  
65 70 75 80

cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta 288  
Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu  
85 90 95

atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc 336  
Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile  
100 105 110

tta aat act acg aat aaa gcc aca gtg aat gtg gtt gca agt gaa	384
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu	
115 120 125	
gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt	432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
130 135 140	
cgg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc	480
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Ser Gly Ala Gly Asn Asn Ala	
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta	528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
165 170 175	
ggc acg aat gat cgt tgg agt ttc tgg agt agt tac cgt tta tat aaa	576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag	624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tgg gaa tct acg tat	672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
210 215 220	
gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc	720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
225 230 235 240	
caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag	768
Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
245 250 255	
agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt	816
Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
260 265 270	
tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc	864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
275 280 285	
gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc	912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
290 295 300 305	
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca	960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
310 315 320 325	
gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt	1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
330 335	
att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat	1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
340 345 350	
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa	1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	

aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt 1152  
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly  
 370 375 380

ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg 1200  
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr  
 385 390 395 400

gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt 1248  
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe  
 405 410 415

att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca 1296  
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr  
 420 425 430

acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta 1344  
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu  
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ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt 1392  
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly  
 450 455 460

gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt 1440  
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu  
 465 470 475 480

tct ttt taatctcttt taagttaag gattaactta atatgaacaa aaatcggtac 1496  
 Ser Phe

aaactcattt ttagtcaagt caaagggtgt ctggttcctg tggcagaatg tattaactca 1556

gctattagca atgggttcac tgattcaaca tccacatcag aacaagtga agaggaaacct 1616

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gataatagcg atcatattaa attagatgca tctaactctg ctggaatga taaaacaaaa 1856

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atttcagata accgttttga aaaatttaatt attccaaata gcgcggtgtt taataataat 1976

gggactgaag cgcaggcaag atcaacatta attggttaca ttccgcaaaa tcaaaattta 2036

aggggagggg aagaagctga tgttatatta aatcaagtga caggtcctca agaaagtaaa 2096

attgttggtg cgcttgaagt attaggtaaa aaagctgata tctgctattg aaaccaaatt 2156

ggtattacct taatgggtg aagaacaata aattcagatc gttttgttgc cactacgagt 2216

gagcttatag atccgaatca gatgatgtta aagggttaca aaggaaatgt gatcattgat 2276

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caaaagcaat caattacatc aggggataat tcagaagcaa aaacagatgt cactcttatt 2396

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<211> 482

<212> PRT

<213> Pasteurella multocida

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Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile  
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His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu  
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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser  
 35 40 45

Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe  
 50 55 60

Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys  
 65 70 75 80

Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu  
 85 90 95

Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile  
 100 105 110

Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu  
 115 120 125

Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe  
 130 135 140  
 Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala  
 145 150 155 160  
 Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu  
 165 170 175  
 Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys  
 180 185 190  
 Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln  
 195 200 205  
 Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr  
 210 215 220  
 Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr  
 225 230 235 240  
 Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu  
 245 250 255  
 Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser  
 260 265 270  
 Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser  
 275 280 285  
 Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser  
 290 295 300  
 Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser  
 305 310 315 320  
 Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser  
 325 330 335  
 Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr  
 340 345 350  
 Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu  
 355 360 365  
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly  
 370 375 380  
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr  
 385 390 395 400  
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe  
 405 410 415  
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr  
 420 425 430  
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu  
 435 440 445  
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly  
 450 455 460

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tggttttgggt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656  
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act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704  
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys  
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aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752  
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu  
25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800  
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln  
40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848  
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 Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu 100  
 gtc tgc tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992  
 Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly 115  
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 Leu Ile Ser Val Asn Ala Thr Arg Leu Asn 125  
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 Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr 45  
 35 40 45  
 His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu 60  
 50 55 60  
 Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile 80  
 65 70 75 80  
 Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn 95  
 85 90 95  
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Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe  
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gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060  
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr  
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Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro  
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atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc 1156  
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Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser  
60 65 70 75  
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc 1252  
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser  
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ggg att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca 1300  
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala

95	100	105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val 110 115 120			1348
ggt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr 125 130 135			1396
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro 140 145 150 155			1444
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile 160 165 170			1492
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Ser 175 180 185			1540
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys 190 195 200			1588
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg 205 210 215			1636
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ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val 300 305 310 315			1924
cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg 320 325 330			1972
ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile 335 340 345			2020

tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068  
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 Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly  
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 Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser  
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 460 465 470 475

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Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu  
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Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala  
 65 70 75 80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp  
 85 90 95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu  
 100 105 110

Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys  
 115 120 125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp  
 130 135 140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val  
 145 150 155 160

Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His  
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Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu  
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Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro  
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Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val  
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Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala  
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Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly  
 245 250 255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro  
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Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala  
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Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile  
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Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala  
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Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile  
 325 330 335

Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala  
 340 345 350

Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu  
 355 360 365

Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser  
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Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp  
385 390 395 400

Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly  
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Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His  
420 425 430

Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala  
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Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly  
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<210> 25

<211> 2364

<212> DNA

<213> Pasteurella multocida

<220>

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<222> (191)..(1828)

<220>

<223> H11501

<400> 25

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aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttggcg 180

gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229  
Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys  
1 5 10

gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277  
Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu  
15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca 325  
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala  
30 35 40 45

aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg 373  
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala  
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caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg 421  
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly

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Ile	Ala	Glu	Pro	Arg	Asn	Ala	Thr	Pro	Gln	Glu	Glu	Lys	Leu	Gln	Val	
		95				100					105					
gaa	att	gac	gag	ctt	ttc	tat	caa	ttc	cca	atg	cta	gaa	gat	tta	atg	565
Glu	Ile	Asp	Glu	Leu	Phe	Tyr	Gln	Phe	Pro	Met	Leu	Glu	Asp	Leu	Met	
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Val	Asp	Met	Met	Asp	Ala	Val	Gly	His	Gly	Phe	Ser	Ala	Leu	Glu	Ile	
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gaa	tg	aag	caa	gct	gaa	agt	aaa	tg	att	cca	gtt	aat	ttt	atc	gca	661
Glu	Trp	Lys	Gln	Ala	Glu	Ser	Lys	Trp	Ile	Pro	Val	Asn	Phe	Ile	Ala	
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Arg	Pro	Gln	Ser	Trp	Phe	Lys	Leu	Asp	Lys	Asp	Asp	Asn	Leu	Leu	Leu	
			160				165					170				
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Lys	Thr	Pro	Asp	Asn	Gln	Asp	Gly	Glu	Pro	Leu	Arg	Gln	Tyr	Gly	Trp	
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gta	gtg	cat	acc	cac	aaa	tca	aga	aca	gta	cag	ctt	gct	cgt	atg	ggg	805
Val	Val	His	Thr	His	Lys	Ser	Arg	Thr	Val	Gln	Leu	Ala	Arg	Met	Gly	
190					195					200				205		
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Leu	Phe	Arg	Thr	Leu	Ala	Trp	Leu	Tyr	Met	Phe	Lys	His	Tyr	Ser	Val	
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His	Asp	Phe	Ala	Glu	Phe	Leu	Glu	Leu	Tyr	Gly	Met	Pro	Ile	Arg	Ile	
			225				230						235			
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Gly	Lys	Tyr	Pro	Phe	Gly	Ala	Thr	Asn	Asp	Glu	Lys	Arg	Thr	Leu	Leu	
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cgt	gca	ctt	gct	caa	atc	gga	cat	aac	gca	gca	ggg	att	atg	cca	gaa	997
Arg	Ala	Leu	Ala	Gln	Ile	Gly	His	Asn	Ala	Ala	Gly	Ile	Met	Pro	Glu	
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Gly	Met	Asn	Val	Glu	Leu	His	Asn	Val	Thr	Asn	Thr	Thr	Gly	Ser	Ala	
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gca	cgt	ttg	att	cta	ggg	caa	aca	tta	aca	agc	ggg	gca	gat	ggg	aaa	1141
Ala	Arg	Leu	Ile	Leu	Gly	Gln	Thr	Leu	Thr	Ser	Gly	Ala	Asp	Gly	Lys	
			305					310					315			

act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac 1189  
Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp  
320 325 330

ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag 1237  
Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln  
335 340 345

att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct 1285  
Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro  
350 355 360 365

tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta 1333  
Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu  
370 375 380

agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc 1381  
Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg  
385 390 395

att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag 1429  
Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln  
400 405 410

gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat 1477  
Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp  
415 420 425

tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa 1525  
Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Thr Ala Leu Ser Val Gln  
430 435 440 445

aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta 1573  
Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu  
450 455 460

tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga 1621  
Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly  
465 470 475

ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca 1669  
Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro  
480 485 490

atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat 1717  
Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp  
495 500 505

gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac 1765  
Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His  
510 515 520 525

gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt 1813  
Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu  
530 535 540

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa 1868  
Gly Gly Thr Asn Val  
545

gccattgagt ttttacataa taaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928

catgatagtg ccacgcgaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988  
 aatgatattt ataaatcaat ggaagttgcc aaaaaagagg gtaagagctt tacacaatgg 2048  
 aaaaaagact tggtaagtga gtttgagaaa aaaggctggg tattcgggca tgataaatct 2108  
 atcagtcgcg gtatcgacgg aaaactgttg gctgatccga aaacaggcga atattttggt 2168  
 acaccgctgc ggctgaatac aatttatcgt acaaactgtc aagccgcata ttctcgcgcg 2228  
 cgctatcagc gcatgatgga taatattgat catcgccctt attgccaata ttccgctgctc 2288  
 agcgatgagc gtacacgacc ctctcatctt gcactaaacg gtcgaattta tcgctatgat 2348  
 gacccgtttt ggtcga 2364

<210> 26  
 <211> 546  
 <212> PRT  
 <213> *Pasteurella multocida*

<400> 26  
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 Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu Thr Gly Arg  
 20 25 30  
 Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys  
 35 40 45  
 Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu  
 50 55 60  
 Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile  
 65 70 75 80  
 Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu  
 85 90 95  
 Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp  
 100 105 110  
 Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met  
 115 120 125  
 Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys  
 130 135 140  
 Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln  
 145 150 155 160  
 Ser Trp Phe Lys Leu Asp Lys Asp Asn Leu Leu Leu Lys Thr Pro  
 165 170 175  
 Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His  
 180 185 190  
 Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg  
 195 200 205

Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe  
 210 215 220  
 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr  
 225 230 235 240  
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu  
 245 250 255  
 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn  
 260 265 270  
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn  
 275 280 285  
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu  
 290 295 300  
 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr  
 305 310 315 320  
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val  
 325 330 335  
 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu  
 340 345 350  
 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val  
 355 360 365  
 Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu  
 370 375 380  
 Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu  
 385 390 395 400  
 Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln Glu Asn Glu  
 405 410 415  
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp  
 420 425 430  
 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val  
 435 440 445  
 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn  
 450 455 460  
 Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln  
 465 470 475 480  
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys  
 485 490 495  
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala  
 500 505 510  
 Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu  
 515 520 525  
 Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr  
 530 535 540

Asn Val  
545

<210> 27  
<211> 1353  
<212> DNA  
<213> Pasteurella multocida

<220>  
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<220>  
<221> CDS  
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<400> 27  
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Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu  
1 5 10 15

ttt tta gaa gat cgc cgt gaa aag ctt acc gaa gaa aaa aca tta 97  
Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu  
20 25 30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145  
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu  
35 40 45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193  
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr  
50 55 60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241  
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
65 70 75 80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289  
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser  
85 90 95

ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337  
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr  
100 105 110

agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385  
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe  
115 120 125

gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt 433  
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe  
130 135 140

cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat 481  
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr  
145 150 155 160

aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg 529  
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met  
165 170 175

gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg 577

Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg	180 185 190	
tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625	
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	195 200 205	
aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tgg	673	
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	210 215 220	
tat caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca	721	
Tyr Gln Leu Ser Leu Gly Tyr Gln Leu His Pro Ser His Gln Ile Ala	225 230 235 240	
tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat	769	
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	245 250 255	
ttt gaa gac cga gga aaa agt tct tca caa ttt ctt cct aac ccc gat	817	
Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	260 265 270	
cta caa ccg gaa act gca ctg aat cat gaa ata agt tac cgt ttc caa	865	
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	275 280	
aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat	913	
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	290 295 300	
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961	
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	305 310 315 320	
tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt	1009	
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe	325 330 335	
gtt aat gaa cct gaa gcc gtg att aaa ggg gtt gaa gta agc ggt gct	1057	
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala	340 345 350	
tta aat ggg tgg gca ttc gga ctt tcc gac ggt tta act ttc cgt ctc	1105	
Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu	355 360 365	
aaa ggg agc tac agc aaa ggt caa aat cat gac ggc gat ccg tta aaa	1153	
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys	370 375 380	
tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa	1201	
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu	385 390 395 400	
ggg tgg agc gtg agt ttg agc ggg cgt tat agt gcg gct aaa aaa gcc	1249	
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala	405 410 415	
aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa	1297	
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys	420 425 430	

caa tgg ccg cat tta agt cca tcc tac ttt gtt gtt gat ttt acg ggg 1345  
Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly  
435 440 445

caa gtt ga 1353  
Gln Val  
450

<210> 28  
<211> 450  
<212> PRT  
<213> Pasteurella multocida

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Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu  
20 25 30  
Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu  
35 40 45  
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr  
50 55 60  
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu  
65 70 75 80  
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser  
85 90 95  
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr  
100 105 110  
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe  
115 120 125  
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe  
130 135 140  
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr  
145 150 155 160  
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met  
165 170 175  
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Arg  
180 185 190  
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile  
195 200 205  
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser  
210 215 220  
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala  
225 230 235 240  
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr  
245 250 255

Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp  
 260 265 270  
 Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln  
 275 280 285  
 Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His  
 290 295 300  
 Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu  
 305 310 315 320  
 Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe  
 325 330 335  
 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala  
 340 345 350  
 Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu  
 355 360 365  
 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys  
 370 375 380  
 Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu  
 385 390 395 400  
 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala  
 405 410 415  
 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys  
 420 425 430  
 Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly  
 435 440 445  
 Gln Val  
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<210> 29  
 <211> 4936  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
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 <222> (1078)..(2769)

<220>  
 <223> hxuC

<400> 29  
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 catggctagc attctagcaa aaattagttg agggaaaatag cggtcttggt ttgcttaaaa 180  
 aacaaccac cccgtagggc acggctgttt ctttttgaga aattacgctt cttcatcttg 240  
 atcttttttc aagatctcat cttcattgag ttttaaaaga cgggcaatcg cattgcggta 300

ggagatttca aggcctttctc gactagtagc aatgacacct tgatcgatta agaaaccgtc 360  
 attgacatca taaacccaac catgtaatga gagtttttcc ccatttttcc acgcggattt 420  
 aatgattgac gagegcacct agttataaac ttgctctgcg acgttaattt tgcgcagcat 480  
 atcagcccggt ttttcaggcg gtaaatgtcc aagtaaatga ctatgcttat accaaatatc 540  
 gcgtaagtgg agtaaccagt tattaattaa acctaatact tgatccgccca ttgcggcgtt 600  
 aattccacca cagtttgtat gtccacaaat aataatgtgt tcaatattta agacctcaac 660  
 ggcatattgc acaacagata aacagtttaa atcgggtgtga atgacttgat ttgcaacatt 720  
 acgatgcaca aacagctcac ccggctcctaa atttgtaaat ttttctgcag gaacacggct 780  
 atccgagcaa ccaatccaaa gatagctcgg ggtttgatga tcagccaatt ctttaaagta 840  
 agaggagttt tctcttttca tccgtaacgc ccagctataa ttattggcaa aaagttgttc 900  
 aatttttttc attagagtga ttctataacc gcaaaaataa gggggctagt atagcttaga 960  
 aatagacagt gggtaagaa aggcacaaaa ttgtatagga taacttgttt tttattgcc 1020  
 tttatttaga attagaatct ttaataataa aaataattat cattaaggtt aatagtt 1077  
 atg gat aaa aat tta atg aag gga tgt gta ttc tta tca ata gtc ggt 1125  
 Met Asp Lys Asn Leu Met Lys Gly Cys Val Phe Leu Ser Ile Val Gly  
 1 5 10 15  
 tgc ggt atc caa ata ggg cta gca tca aat cca aat cct cca gat gtg 1173  
 Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val  
 20 25 30  
 gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221  
 Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu  
 35 40 45  
 cca ggt cgt tct gta tta aaa cag aaa aat atc gat caa caa caa gca 1269  
 Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala  
 50 55 60  
 gat aat gcc gct gac tta ata aat att tta cct ggg gta aat atg gcg 1317  
 Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala  
 65 70 75 80  
 gga gga ttt cgc cct ggt ggt caa aca tta aat att aat gga atg ggt 1365  
 Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly  
 85 90 95  
 gat gct gaa gat gtt aga gtt caa cta gac ggc gca aca aat gtt ttc 1413  
 Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe  
 100 105 110  
 gaa aaa tat caa caa ggc tct att ttt att gaa cct gag tta tta aga 1461  
 Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg  
 115 120 125  
 aag gtg aca gta gac aaa gga aat tat tct cct caa tat ggc aat ggt 1509  
 Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Tyr Gly Asn Gly  
 130 135 140

ggc ttt gct ggt act gta aaa ttt gaa aca aaa gat gca act gat ttt 1557  
 Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe 160  
 145 150 155

ttg aaa gaa aat cag aaa ata ggt gga tta ttt aaa tat gga aat aat 1605  
 Leu Lys Glu Asn Gln Lys Ile Gly Gly Leu Phe Lys Tyr Gly Asn Asn 175  
 165 170

agc aat aat aac caa aaa act tat agt aca gcc cta gtt tta cag aat 1653  
 Ser Asn Asn Asn Gln Lys Thr Tyr Ser Thr Ala Leu Val Leu Gln Asn 190  
 180 185

gaa caa aaa aat att gat ttg tta tta ttt ggt tct gta aga aat gca 1701  
 Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala 205  
 195 200

agc aat tat aca aga cct gat aaa agt aaa att ctt ttt tca aaa aac 1749  
 Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn 220  
 210 215

aat caa aaa agt gga tta ata aaa gta aat tgg caa att act cct gaa 1797  
 Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu 240  
 225 230 235

cat tta tta act tta tcc agt gtt tat ggc att cat aaa ggg tgg gaa 1845  
 His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu 255  
 245 250

cct tgg gca gca aaa aga gat gtg atg tgg aga cca aca gaa aca gaa 1893  
 Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu 270  
 260 265

ata aaa cac tat ggg att gat gtt gcg tgg aaa cgt aaa ctt gtt tat 1941  
 Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr 285  
 275 280

cga gat caa aaa gat gaa agt tat tca ttg aaa tat cgc tat tta cct 1989  
 Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro 300  
 290 295

gaa aat aat aag tgg att aat ttg tct gtt cag ctg agt tat agt aaa 2037  
 Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys 320  
 305 310 315

aca gag cag aat gat act cgc cat gag aaa gtc act tct tca ttc cta 2085  
 Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu 335  
 325 330

ggt aca tta gga aat aaa agt tgg ata act tat tca gat ctt act ttt 2133  
 Gly Thr Leu Gly Asn Lys Ser Trp Ile Thr Tyr Ser Asp Leu Thr Phe 350  
 340 345

gat ata agt aac aca agt act cta aat att ggg cgt gct gag cat gaa 2181  
 Asp Ile Ser Asn Thr Ser Thr Leu Asn Ile Gly Arg Ala Glu His Glu 365  
 355 360

cta cta ttt ggt tta cag tgg tta aaa aat aaa aga aat acc ctt atg 2229  
 Leu Leu Phe Gly Leu Gln Trp Leu Lys Asn Lys Arg Asn Thr Leu Met 380  
 370 375

tat cat aaa ggg gga gtc aag aag gca gac tat aat tat ggc tat ttt 2277  
 Tyr His Lys Gly Gly Val Lys Lys Ala Asp Tyr Asn Tyr Gly Tyr Phe

385		390		395		400	
cag cct tat	tat atg cct tct gga cgc cag tat	aca caa gca ttt tat	2325				
Gln Pro Tyr	Tyr Met Pro Ser Gly Arg Gln Tyr Thr	Gln Ala Phe Tyr					
	405	410					
tta caa gat	caa ata aaa tgg cag aat ttc ctc	ttt aca gga ggg ata	2373				
Leu Gln Asp	Gln Ile Lys Trp Gln Asn Phe Leu Phe	Thr Gly Gly Ile					
	420	425			430		
aga tat gac	cat atc aat aat ata ggg cag aaa aat	tta gcg cca cga	2421				
Arg Tyr Asp	His Ile Asn Asn Ile Gly Gln Lys Asn	Leu Ala Pro Arg					
	435	440			445		
tat aat gat	atc tct gca gga cat gat tat agc cag aaa aat	tat aat	2469				
Tyr Asn Asp	Ile Ser Ala Gly His Asp Tyr Ser Gln Lys Asn Tyr Asn						
	450	455			460		
ggg tgg tct	tat tat tta ggt ctt aag tat gat gta aat cat	tat tta	2517				
Gly Trp Ser	Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu						
	465	470			475		
agt tta ttt	acg aat ttt agt aaa act tgg cga gcc cct gtt att gat		2565				
Ser Leu Phe	Thr Asn Phe Ser Lys Thr Trp Arg Ala Pro Val Ile Asp						
	485	490			495		
gaa cag tat	gag aca caa tat agt caa gct tct gta tct gcg act tct		2613				
Glu Gln Tyr	Glu Thr Gln Tyr Ser Gln Ala Ser Val Ser Ala Thr Ser						
	500	505			510		
tta aat tta	gaa aaa gaa atg att aat caa acc aga gtg ggt gga att		2661				
Leu Asn Leu	Glu Lys Glu Met Ile Asn Gln Thr Arg Val Gly Gly Ile						
	515	520			525		
att act ctc	aat cat cta ttt cag gaa aat gat gct ttt caa ttt aga		2709				
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Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu	35	40	45
Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala	50	55	60
Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala	65	70	75
Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly	85	90	95
Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe	100	105	110
Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg	115	120	125
Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Gln Tyr Gly Asn Gly	130	135	140
Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe	145	150	155
Leu Lys Glu Asn Gln Lys Ile Gly Gly Leu Phe Lys Tyr Gly Asn Asn	165	170	175
Ser Asn Asn Asn Gln Lys Thr Tyr Ser Thr Ala Leu Val Leu Gln Asn	180	185	190
Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala	195	200	205
Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn	210	215	220
Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu	225	230	235
His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu	245	250	255
Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu	260	265	270
Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr	275	280	285
Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro	290	295	300
Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys	305	310	315
Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu	325	330	335

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His Gln Glu Ala Thr Glu Leu Asp Thr Ile Thr Val Ser Ser Gln Gln  
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Asp Glu Met Asn Ile Lys Glu Lys Lys Ile Gly Glu Thr Val Lys Thr  
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Val Asp Gly Leu His Gln Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys  
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 190 195 200

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 Arg His Gly His Glu Leu Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp  
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 Phe Thr Val Ala Ser Asp Thr Tyr Leu Gln His Ser Arg Gly His Asp  
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ctt tca tat aat ctt gtt gca aca aca cat att cag tta gat gag aaa 5655  
 Leu Ser Tyr Asn Leu Val Ala Thr Thr His Ile Gln Leu Asp Glu Lys  
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Leu Gln Gly Ser Gly Leu Ser Thr Gln Ile Val Asp Glu Asn Gly Lys			
380	385	390	
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Leu Arg Leu Arg Pro Thr Gly Phe Trp Leu Asp Cys Ser Val Phe Asp			
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Cys Asn Lys Pro Phe Thr Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln			
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Ala Arg Glu Val Leu Leu Ser Glu Glu Ile Thr Val Asp Gly Lys Leu			
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Val His Asn Met Ile Ser Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile			
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Lys Tyr Asn Pro Glu Tyr Thr Gly Val Thr Pro Lys Ile Pro Asp			
	605	610	615

gat atg gta aaa ggt ttg ttt att cct atg cca aaa gag cca cag cta Asp Met Val Lys Gly Leu Phe Ile Pro Met Pro Lys Glu Pro Gln Leu 620 625 630	6663
aag gat ttt gat tat aac tat gct aaa ttt ggt gag gcc tat aaa aaa Lys Asp Phe Asp Tyr Asn Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys 635 640 645 650	6711
tgga aaa gaa tat ctg cca aaa aat gcg gaa gaa aat att gct tac att Trp Lys Glu Tyr Leu Pro Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile 655 660 665	6759
gct caa gat aag aca ttt aaa aaa cat tct tat tct ctt ggt gca act Ala Gln Asp Lys Thr Phe Lys Lys His Ser Tyr Ser Leu Gly Ala Thr 670 675 680	6807
ttc gat cct ctg aat ttt tta cga gta caa gta aaa tat tca aaa ggg Phe Asp Pro Leu Asn Phe Leu Arg Val Gln Val Lys Tyr Ser Lys Gly 685 690 695	6855
ttt aga gcc ccg act tcg gat gaa ctt tat ttt acc ttt aag cat cca Phe Arg Ala Pro Thr Ser Asp Glu Leu Tyr Phe Thr Phe Lys His Pro 700 705 710	6903
gat ttt acg att tta ccg aac ccc gtg ttg aaa cca gag gaa gca aaa Asp Phe Thr Ile Leu Pro Asn Pro Val Leu Lys Pro Glu Glu Ala Lys 715 720 725 730	6951
aat caa gag att gca tta aca gtg cac gat aat tgg gga ttt gtt agc Asn Gln Glu Ile Ala Leu Thr Val His Asp Asn Trp Gly Phe Val Ser 735 740 745	6999
aca agt gtt ttc caa aca aag tat cgt cat ttt att gat tta gcg tat Thr Ser Val Phe Gln Thr Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr 750 755 760	7047
tta ggt tca aga aat tta tcg aat tcc gtg gga ggg cag gca caa gca Leu Gly Ser Arg Asn Leu Ser Asn Ser Val Gly Gly Gln Ala Gln Ala 765 770 775	7095
aga gat ttc caa gtt tat caa aat gtc aat gtc gat aat gcc aaa gtt Arg Asp Phe Gln Val Tyr Gln Asn Val Asn Val Asp Asn Ala Lys Val 780 785 790	7143
aaa gga ctt gaa att aat gca cgt ttg aat ttg gga tat ttt tgg cat Lys Gly Leu Glu Ile Asn Ala Arg Leu Asn Leu Gly Tyr Phe Trp His 795 800 805 810	7191
gtg ttg gat gga ttt aat acg agc tat aaa ttc act tac caa cgt ggt Val Leu Asp Gly Phe Asn Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly 815 820 825	7239
cgt ttg gat ggc gat cgt cca atg aat gcg att cag cct aaa gct tct Arg Leu Asp Gly Asp Arg Pro Met Asn Ala Ile Gln Pro Lys Ala Ser 830 835 840	7287
gtt ttt ggt ttg ggc tac gat cat aaa gaa aat aaa ttt ggc gct gat Val Phe Gly Leu Gly Tyr Asp His Lys Glu Asn Lys Phe Gly Ala Asp 845 850 855	7335
tta tat att aca cgt gtg agt gag aaa aaa gcg aaa gac act tat aat Leu Tyr Ile Thr Arg Val Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn	7383

860

865

870

atg ttc tat aaa gaa cag gga tat aaa gat agt gct gtt cgt tgg aga 7431  
Met Phe Tyr Lys Glu Gln Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg 890  
875 880 885

agt gat gac tat acg cta gtt gat gcg gtt ggt tat att aaa ccg att 7479  
Ser Asp Asp Tyr Thr Leu Val Asp Ala Val Gly Tyr Ile Lys Pro Ile 905  
895 900

aag aat tta acg tta cag ttt ggc gtt tat aat ttg aca gac cgt aaa 7527  
Lys Asn Leu Thr Leu Gln Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys 915  
910 920

tac ttg aca tgg gaa tct gct cgt tgc att aaa cca ttt ggt aca agt 7575  
Tyr Leu Thr Trp Glu Ser Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser 935  
925 930

aat tta att aat caa aaa aca ggc gca gga att aat cgt ttt tac tca 7623  
Asn Leu Ile Asn Gln Lys Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser 945  
940 950

cca ggt cgt aac ttt aaa ctc agt gcc gaa atc acc ttc taatcctaag 7672  
Pro Gly Arg Asn Phe Lys Leu Ser Ala Glu Ile Thr Phe 965  
955 960

ctcgcgtatg caggctttct ttttagggaa agtgcggtgg atttgacaaa gatttattgc 7732

ttttctgtaa atcaatgcta aaattcacac tcctttgtcg tagctggatt agagatcggc 7792

tagcgatgta tttttaactt aacttttagg agttatcaaa tgtctctaaag tacagaaaaa 7852

aaagcagcaa ttgttgctga atttggtcgt gatgcaaaag ataccgggttc ttcagaagtg 7912

caaatcgcat tattaactgc acaaatcaac cacttacaat ctccactttgc aacgcacaaa 7972

aaagaccacc acggtcgtcg tgggtttattg cgtatgggtt ctgcgtcgta taaactttta 8032

gattacttaa aacgtactaa tcttgagcct tacacttcaa ctatcgctcg ttttaggttta 8092

cgctgctaatt ttgtattagg atttattcca aacaaaaaac ccttgataat tttatcaagg 8152

gtttctcttt ttctgcatac taggcatggt taaattatcg caaaacacac cgcacatttc 8212

gtggaaaagt goggtcattt ttttaattta ttttacttct ttaaactatga tctcacttgg 8272

gattactgaa ccttgccagt aaagctcagt agcgactttt tcagctaatt gcataaacga 8332

ttgggcaatg tcgctttcag gtgcggcgac aacgggttggg atacctttgt ctaaaatttc 8392

acgtaagcga atatgtaatg cctgttgtcc taaaactttg acattatatt tttgtgcaat 8452

gcgctcagca ccgcctgttc cgaaaatcgt ttcttgatga ccacaattgc tacaatatg 8512

catcgacata ttttcgataa tgcctaaaaac gggtacagaa acacgctcaa acatcgccac 8572

acctttaatc gcatccagta aagcaatatc ttgtggtggt gtcaccacga ccgccccgt 8632

cactggaatt ttgtgagaaa gggtcagctg gatattccct gtaccccggtg gcatatcaat 8692

gactaaataa tctaatacag gccataaggt ttcttgcaaa agctgactta aggcactgct 8752

tgccattgga ccgcgcaaaa tcgtagcatt gtccggttcc attaagaac caatggaatt 8812  
 ggcaaaaata tgatgtgctt gaattggggt aatgtgctgg ttatctggcg aagttgggcg 8872  
 ttgatcagca acccctaaca tgttggaat agatggacca taaatatcgg catctaaaat 8932  
 tccaacacga gcacctgtgc tttgtaaggc aagagcaaga ttgacggaaa tagtagattt 8992  
 tcctacacca cctttaccgc atgtcacggc aataatattt ttaccocctt ttacggctgg 9052  
 gtggctatta gcgcgtttta atgtcgcgat ttgataattt aattgccatt tgatgtcttt 9112  
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 tgattttatc ccgttatttt tgggtgctaa ttaaagccct agttaatcac tcaactatat 9412  
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 aaaatactgc gaataaggta acataagcgc caattttttg atgaaaata ggaatgataa 9532  
 catggcaaat tcggcacgcg atattttggt cacttgccgc ttacctatg caaatgggtc 9592  
 aattcattta gggcatttat tagaacatat tcaagcagat attgggtgc gttccaacgt 9652  
 atgcgtgggc ataaagtgca ttttatttgt gcagatgatg cccatggcac accaatcatg 9712  
 ttaaatgcga taaattaggt attacaccaa agcattaatt gtcctctgaa agcagaacat 9772  
 gtggcggatt tgaaggctta atattagcta tgataatatc at 9814

<210> 32  
 <211> 967  
 <212> PRT  
 <213> Pasteurella multocida

<400> 32  
 Met Arg Thr Thr Thr Ile Lys Phe Ser Ala Ile Thr Leu Ala Leu Leu  
 1 5 10 15  
 Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser His Gln Glu Ala Thr Glu  
 20 25 30  
 Leu Asp Thr Ile Thr Val Ser Ser Gln Gln Asp Glu Met Asn Ile Lys  
 35 40 45  
 Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg  
 50 55 60  
 Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val  
 65 70 75 80  
 Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg  
 85 90 95  
 Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln

100

105

110

Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr		
115	120	125
Gly Asn Phe Asn Asn Thr Arg Asn Ser Val Glu Ile Glu Thr Leu Lys		
130	135	140
Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly		
145	150	155
Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe		
165	170	175
Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr		
180	185	190
Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln		
195	200	205
Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu		
210	215	220
Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg		
225	230	235
Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys		
245	250	255
Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp		
260	265	270
Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val		
275	280	285
Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn		
290	295	300
Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr		
305	310	315
Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg		
325	330	335
Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu		
340	345	350
Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln		
355	360	365
Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu		
370	375	380
Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr		
385	390	395
Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr		
405	410	415
Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr		
420	425	430

Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu  
 435 440 445  
 Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu  
 450 455 460  
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr  
 465 470 475 480  
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln  
 485 490 495  
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn  
 500 505 510  
 Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile  
 515 520 525  
 Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg  
 530 535 540  
 Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro  
 545 550 555 560  
 Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr  
 565 570 575  
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser  
 580 585 590  
 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr  
 595 600 605  
 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu  
 610 615 620  
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn  
 625 630 635 640  
 Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro  
 645 650 655  
 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe  
 660 665 670  
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe  
 675 680 685  
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser  
 690 695 700  
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro  
 705 710 715 720  
 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu  
 725 730 735  
 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr  
 740 745 750  
 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu  
 755 760 765

Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr  
 770 775 780  
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn  
 785 790 795 800  
 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn  
 805 810 815  
 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg  
 820 825 830  
 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr  
 835 840 845  
 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val  
 850 855 860  
 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln  
 865 870 875 880  
 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu  
 885 890 895  
 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln  
 900 905 910  
 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser  
 915 920 925  
 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys  
 930 935 940  
 Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys  
 945 950 955 960  
 Leu Ser Ala Glu Ile Thr Phe  
 965

<210> 33  
 <211> 2990  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1106)..(1564)

<220>  
 <223> kdtB

<400> 33  
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 tgggtgccga accgcgccag ggactttgtt ataaacggtt tgataacgtt ttttatccgc 120  
 ttcttcgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaaacac 180  
 gtctaaaagt gcggctctgtt tttcgcgat ttctaattca aataaggtat catggcgcgcc 240  
 aaccatgatc attttgacac catgatgttc acctaaacta tcttcgccta accacagttc 300



tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564  
Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn  
140 145 150

taagagttag gtgaagaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624  
tctaaaaatc aattcactct gaaagggtag gaatgcgtag attcctctatt tcaagcatgc 1684  
agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaaaataa ggaaagagat 1744  
attttttatg gtcatattg tttatccttt caatctattt atttattacc atacaagaaa 1804  
gacgagggtta ttgttttgac aaatgggaat ataccataa cctttatacc gagcaagagt 1864  
tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcagggtgtt tttgaaccag 1924  
atggcacaac aaccgaaata aaacgttatg ctagtgttga ggagtttaaa cagatgaacc 1984  
ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044  
atggatatgg ttatataaga attgaatatt taagacatta tgttgggaat tttaaacctg 2104  
atcatagagt gctttatctc gaatatacgc cttgtggaga attaaggga gaggtttctt 2164  
tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224  
aaatgcata tttatataaa ataaattaac tcctaaagcg gaggaagag tagattcaat 2284  
acaaattctt gaaaaggag atgaacattt cgaagtaaat ttaattgat caaagtactc 2344  
tattgatga aggaaaaaca gtggaattaa tggcaggtag ggcagttctt gcggaatta 2404  
aaacaggtaa acgcagtgtt ttagattact tatttagccc attaaaaacc aaaaataat 2464  
attaaggaga ataatatgtc gtataataaa tatactgttg ctttgattac gttctcaaca 2524  
gggatctgta ttccggcaat atgtacgct ctaaattcgc tgggatacag atcctgtttg 2584  
agactatgta gaaaagacta aactttgtgt gggttaactg gcttcggtaa aattctgtaa 2644  
acaaatgggc ttaaccgcgc tgatcttato ccgtgagctt tcgcttgatg aaattgccga 2704  
aattcgtcag caagtgccag aaatggaaat tgaagtgttc gtgcattggg cattatgcatt 2764  
ggcgtattct ggacgtgtgt tattatcagg ctatattaat aaacgtgatc caaatcaagg 2824  
cacctgtacc aatgcgtgcc gttgggaata cagtgttaacc gaagccaaag aagatgagat 2884  
cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaat aatgtagcac cgacacttgg 2944  
cgaaggcgac accaccagta aagtattttt attagcagaa agtcga 2990

<210> 34  
<211> 153  
<212> PRT  
<213> Pasteurella multocida

<400> 34  
Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu  
1 5 10 15

Phe Ile Leu Ser Ile Tyr Leu Phe Ile Thr Ile Gln Glu Arg Arg Gly  
                     20                    25                    30  
 Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln  
                     35                    40                    45  
 Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser  
                     50                    55                    60  
 Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr  
                     65                    70                    75                    80  
 Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr  
                     85                    90                    95  
 Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Tyr  
                     100                    105                    110  
 Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys  
                     115                    120                    125  
 Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu  
                     130                    135                    140  
 Arg Glu Glu Ala Ala Phe Ser Lys Asn  
 145                    150

<210> 35  
 <211> 1683  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (325)..(1230)

<220>  
 <223> lgtC

<400> 35  
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 tgggtattat tcataggcta ggtgaaagat atatttttcc atgatattaa aacgattcag 120  
 gcagaactgg cttagcttacc acttttagat aattgtatta ttaaaagaag ctgtatgatt 180  
 gttattctat cattagtggg taataaatat tctttatttt ttgagagata aaaacaattc 240  
 atatttcaat agaaaaacaga aaataaagat tatcaaaaga attatccgctc cttataaata 300  
 tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351  
                     Met Asn Ile Leu Phe Val Ser Asp Asp  
                     1                    5  
 gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399  
 Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His  
                     10                    15                    20                    25  
 aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447  
 Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp  
                     30                    35                    40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa	495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu	
45 50 55	
gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt	543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val	
60 65 70	
caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca	591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala	
75 80 85	
gag tat ttg cgg gat aat tta aat aaa att att tat tta gat gtt gat	639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp	
90 95 100 105	
gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat	687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn	
110 115 120	
aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag	735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys	
125 130 135	
tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt	783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe	
140 145 150	
aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat	831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp	
155 160 165	
gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg	879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met	
170 175 180 185	
att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc	927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val	
190 195 200	
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga	975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg	
205 210 215	
ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa	1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu	
220 225 230	
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa	1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys	
235 240 245	
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa	1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys	
250 255 260 265	
ata tta gca naa atn tcg aga gcc ncg gat aaa gaa cgc gta tta tct	1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser	
270 275 280	
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc	1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe	

aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc 1270  
 Lys Tyr Gln Val Tyr  
 300

tgattttctc aaagcgaaaa ggaggaaata gcttggttcta atttattaca ataatggttg 1330  
 tattcatctt gattttgaag gaaagagagt gttttttgta taaagcatt ttcgtcacct 1390  
 aaatttacta atcctccaaa ttctcctcct cgnagaattt ctttcggacc ggtagggcag 1450  
 tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaaacccc 1510  
 tctttcaaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570  
 ttatttccta aaagaaaaca atcttcttgt agattgagtg attctatttg ttctctaat 1630  
 ttctctcgac actcaccatc ccaacaata tatancnttt ctggatacc tcc 1683

<210> 36

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 36

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val  
 1 5 10 15

Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 20 25 30

Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 35 40 45

Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 50 55 60

Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 65 70 75 80

Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
 85 90 95

Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
 100 105 110

Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
 115 120 125

Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
 130 135 140

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 145 150 155 160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 165 170 175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 180 185 190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 195 200  
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly  
 210 215 220  
 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Met Pro Val Val  
 225 230 235 240  
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 245 250 255  
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg  
 260 265 270  
 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala  
 275 280 285  
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr  
 290 295 300

<210> 37  
 <211> 2029  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (2)..(499)

<220>  
 <223> mglB

<400> 37  
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 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln  
 1 5 10 15

gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97  
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu  
 20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145  
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met  
 35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193  
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser  
 50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241  
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met  
 65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289  
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro  
 85 90 95

atc ttc ngg gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337  
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys  
 100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385  
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys  
 115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433  
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr  
 130 135 140

gaa ggc aca aaa tgg cag tta aaa cga tgc tgt cct acg tat ccc tta 481  
 Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu  
 145 150 155 160

tgt tgg tgt gga tgc gga taacttaaac gagttcctaa aataataaac 529  
 Cys Trp Cys Gly Cys Gly  
 165

tataacaaaa caagamgttg taattctcgg ggaggtatcac cctccccctt tttatgtgag 589  
 gtgggatatg acaactcaaa ttccaaatca agacagtcaa atactgtcca caatgaccaa 649  
 cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709  
 gcattctgtc catgccttaa tgggacgaaa tggggcgggc aaatcgacct tattaaaatg 769  
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 aaacgccatc acaaaaaccna tattggntca ntatctgggg tggtaaccaa caaaaagtgg 1849  
 tcattggctg ttggttatta acccaccctg aaatcttgat gttagacgaa ccaacacgtg 1909

gtatcgacat tgggtcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969  
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<210> 38  
<211> 166  
<212> PRT  
<213> *Pasteurella multocida*

<400> 38  
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Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu  
20 25 30  
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met  
35 40 45  
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser  
50 55 60  
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met  
65 70 75 80  
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro  
85 90 95  
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys  
100 105 110  
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys  
115 120 125  
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr  
130 135 140  
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu  
145 150 155 160  
Cys Trp Cys Gly Cys Gly  
165

<210> 39  
<211> 2628  
<212> DNA  
<213> *Pasteurella multocida*

<220>  
<221> CDS  
<222> (326)..(766)

<220>  
<223> mioC

<400> 39  
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agaaatttta gatcagttag aagaaaaaat taaacaagcg gttgaaacta tccaattact 120



ctgaaaatta tgatgttatt gtgatcggtg gtggacacgc aggtactgaa gctgcacttg 1326  
 caccggcacg catgggactc aagacctat tattaaccca taatgttgat acactagggc 1386  
 aaatgtcttg taatcctgcg attggtggga ttggtaaagg ccatttagtc cgagaaattg 1446  
 atgcatggg cggtttaatg gcaactgctg cggaccaagc aggaatccaa ttcgtacct 1506  
 taaacagcag caaaggaccg gcggtacgtg ctacacgtgc gcaagctgac cgcgttttat 1566  
 atcgccaagc agtacgtatt gcattagaaa atcaagaaaa tttagatatt tttcaacaag 1626  
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 acattggttt agaaaattat acaggtggac gcgcgggtga tctgcttca gtgatgttag 1806  
 cgcgtggtt aagagaactg aatttacgtg tanatggtt aaaaacgggt acaccgccc 1866  
 gtattgatgc acgtactatt gatttctcaa tactggctaa acaacatggc gatgaaaaat 1926  
 tacctgtctt ttccttcgat ggcattgttg atcaacccc acgtcaaatt ccattgttta 1986  
 ttaccctatac aaatgaaca acgcatgaag tgatccgtaa taacttacat cgcagcccaa 2046  
 tgcgtgctg gatcattgaa ggcgtcggtc cagcttattg ccctcttatt gaagataaag 2106  
 taatgcgtt tctgagcgt aattctcatc aaatctacct tgaacctgaa ggggtgacaa 2166  
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 cgaaatggca aagaaaaacc gcaatcaagc gttgattgca ggtggtattg gcggtggcat 2286  
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 atcagcaagt aaagctaaag tctcatttaa caccgcgca cgtggaaga aagagggcgc 2466  
 aagcaagggc gatgactggg ataaagtgcg tgatgtacaa gtaatggcgg gcaatgagct 2526  
 gactgatatc acaaaaggat tgttatcggg ctttattatt caatatcgcg caaccatgga 2586  
 tgagattcaa aactcgatt taaaagcaca agataaagtc ga 2628

<210> 40

<211> 147

<212> PRT

<213> *Pasteurella multocida*

<400> 40

Met Lys Thr Lys Ile Cys Ile Ile Thr Gly Ser Thr Leu Gly Gly Ala  
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Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Asp Tyr  
 20 25 30

Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu  
 35 40 45

Lys Cys Trp Leu Val Val Thr Ser Thr His Gly Ala Gly Glu Leu Pro  
 50 55 60  
 Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln  
 65 70 75 80  
 Leu Ala Asp Leu Arg Phe Ala Val Ile Gly Leu Gly Asn Ser Asp Tyr  
 85 90 95  
 Asp Thr Phe Cys His Ala Val Asp His Val Glu Gln Leu Leu Ser  
 100 105 110  
 Lys Asp Ala Leu Gln Leu Cys Glu Ser Leu Arg Met Asp Met Leu Thr  
 115 120 125  
 Ile Thr Asp Pro Glu His Thr Ala Glu Gln Trp Leu Pro Gln Phe Leu  
 130 135 140  
 Ser Gln Leu  
 145

<210> 41  
 <211> 5191  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (3203)..(4255)

<220>  
 <223> mreB

<400> 41  
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 ggttggttac acggattaat ggcacgactt cagcggcacc acaagctact ttactgtcga 120  
 tagcgggttaa ttgggcagat ttactctttg gtactatcac agcacacacg ccgctgcat 180  
 ccgcagtagc caaacaagca cctaagttat gtggatcagt cacaccatct aacactaata 240  
 gcaacggatt ggactgattt tgtaaaagcg tatctaaatc tgcttcattc aattctttcg 300  
 ctggctgaac acgtgccatg atgccttggt gtacttcgcc ctctgctttt ttatcaaggg 360  
 tttggcgatt aacaatttgg atagtaatac ccaaccgatg aagttcattg agcaaagggt 420  
 gtaaacgttt atcgtgcgcg cctttgagtg cataaacttc aattaaacg cctggcgcgt 480  
 tgtttaaaaa ggcacttact gcatgaatgc cataaatatt ttcactatc tactttctct 540  
 ttttagctga tttcttactg gcttttttcg tggttgttga tggtttaaca acgcttgttt 600  
 ttcttacgcg acttttactg gtgcttggtt taogtttatg gcgttggttt tcgagacttt 660  
 cagcgtagcg tgcatttttc ttgagcttgt ctttggctgt tttgccttct cgtaatgggt 720  
 tacgctcact cgacactaaa gaaaaatcoa cttggcgttg ttcaaggcta actgcttcca 780  
 cacggatttt taccttatcg ccaatgcggt agatcatacc actattttca ccgattaaac 840

ttgtcgagc gagatcaaat tggtagtagt cgttatctaa ggtagaaatg tggactaagc 900  
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 tggaccgcga tgaatacagga aaagggctgg ctcttgatgt tttccataa agtttgccgc 1500  
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acccaattgt	ccgtcatattt	ccatcgctct	taagcgacgg	cgcattggctt	cttgttgctc	2760
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tacatttttt	gatacattta	gcacaatttt	tcaatactca	aatcagagtg	tccattattt	3180
aatttagttc	agcggaaattc	tt atg	tta ttt	aaa aaa	att cga ggc	tta ttt
		Met Leu	Phe Lys	Lys Ile	Arg Gly	Leu Phe
		1		5		10
tca aat gat	ctg tcc atc	gat ctt ggc	aca gcg	aat acc	tta att	tat
Ser Asn Asp	Leu Ser Ile	Asp Leu Gly	Thr Ala Asn	Thr Thr Leu	Ile Ile Tyr	
		15		20		25
gtc aaa gga	caa ggg att	gtt tta gat	gaa cct	tct gtt	gtg gcg	att
Val Lys Gly	Gln Gly Ile	Val Leu Asp	Glu Pro Ser	Val Val Ala	Ile Ala Ile	
		30		35		40
cgc caa gaa	cgt tca ggt	gca tta aaa	agc att	gct gcg	gtt ggt	cgt
Arg Gln Glu	Arg Ser Gly	Ala Leu Lys	Ser Ile Ala	Ala Val Gly	Arg Arg	
		45		50		55
gat gcc aaa	tta atg tta	ggc cgt	aca ccg	aaa agc	att gca	gcg att
Asp Ala Lys	Leu Met Leu	Gly Arg Thr	Pro Lys Ser	Ile Ile Ala	Ala Ala Ile	
		60		65		70
cgt cct atg	aaa gat ggg	gtg atc gca	gat ttc	ttt gtg	aca gaa	aaa
Arg Pro Met	Lys Asp Gly	Val Ile Ala	Asp Phe Phe	Val Thr Glu	Lys Lys	
		75		80		85
atg ttg caa	tat ttt att	aaa caa	gtg cac	agc agc	aat ttt	atg cgt
Met Leu Gln	Tyr Phe Ile	Lys Gln Val	His Ser Ser	Asn Phe Met	Arg Arg	
		95		100		105
cca agt cca	cgt gtc tta	gtt tgt gta	cct gcg	gga gct	acg caa	gtc
Pro Ser Pro	Arg Val Leu	Val Cys Val	Pro Ala Gly	Ala Thr Gln	Val Val	
		110		115		120
gaa cga cgt	gca atc aaa	gaa gaa	tct gcc	att ggt	gct ggg	gca cgc
Glu Arg Arg	Ala Ile Lys	Glu Ser Ala	Ile Ile Gly	Ala Gly Ala	Arg Arg Glu	
		125		130		135
gtg tac ttg	att gag gaa	ccg atg	gcg gca	gcg att	ggg gct	aaa tta
Val Thr Leu	Ile Glu Glu	Pro Met Ala	Ala Ala Ala	Ile Ile Gly	Ala Lys Leu	
		140		145		150
cct gtt tcg	act gcc aca	ggg tcg	Met Met	gat atc	ggg ggt	ggg
Pro Val Ser	Thr Thr Gly	Ser Met Val	Ile Asp Ile	Arg Ile Gly	Gly Gly Gly	
		155		160		165
acg acg gaa	gtt gcg gtg	att tct	tta aat	ggc att	gtg tat	tcc tct
Thr Thr Glu	Val Ala Val	Ile Ser Leu	Asn Gly Ile	Val Thr Val	Ser Ser Ser	
		170		175		180

	175	180	185	
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat				3808
Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr				
	190	195	200	
gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt				3856
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg				
	205	210	215	
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc				3904
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val				
	220	225	230	
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt				3952
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg				
	235	240	245	250
tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg				4000
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro				
	255	260	265	
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa				4048
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln				
	270	275	280	
cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt				4096
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly				
	285	290	295	
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc				4144
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Ser Lys Glu Thr				
	300	305	310	
ggg gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt				4192
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg				
	315	320	325	330
ggg ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att				4240
Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile				
	335	340	345	
ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt				4295
Phe Ser Asp Asp Ile				
	350			
tacttctctt ttattgctga caaggctagc ctaattcgta tatgaacct atttttggaa				4355
aagcacctcc tttaggtctt cgtttaattc tggcgatttt agcatccatt gcattgattg				4415
tttcggacgg tcaatccaat gcgatgatta aagcacgcag tattatggaa accgcagtag				4475
gcgggctgta ttatcttgcc aatacaccca gaacggtatt ggatgggggt tcagataaatt				4535
tggttgatgc caataaattg caaattgaaa accgagtttt gcgtgatcaa ctgcgtgaaa				4595
aaaatgcaga ttattgttg ttagatcaac tcaaagtaga aaatcaacgc ctgcgcttat				4655
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aaactgatgt gtatcgtaag caagtcgta ttaaccaagg acaacgtgac ggtgcttatg				4775

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 gtaatgatgt ccgttttgatt gctagtggaa caggacggaa tgatgaactg agttagatc 4955  
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 ggcgtttttt agaagggtat cctgttgcca ttgtggaatc cgtatcacgt gatgggcaaa 5075  
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<210> 42  
 <211> 351  
 <212> PRT  
 <213> Pasteurella multocida

<400> 42  
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 Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr Val Lys Gly Gln Gly Ile  
 20 25 30  
 Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly  
 35 40 45  
 Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu  
 50 55 60  
 Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly  
 65 70 75 80  
 Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile  
 85 90 95  
 Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu  
 100 105 110  
 Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys  
 115 120 125  
 Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu  
 130 135 140  
 Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr  
 145 150 155 160  
 Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val  
 165 170 175  
 Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly  
 180 185 190  
 Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly  
 195 200 205  
 Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly  
 210 215 220

Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His  
 225 230 235 240

Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser  
 245 250 255

Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala  
 260 265 270

Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp  
 275 280 285

Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Glu Ala Leu Ile Arg  
 290 295 300

Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile  
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 Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg  
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atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct 144  
 Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala  
 35 40 45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc 192  
 Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile  
 50 55 60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc 240  
 Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile  
 65 70 75 80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca 288  
 Val Arg Ser Arg Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr  
 85 90 95

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Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg	
100 105 110	
aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct	384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala	
115 120 125	
gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta	432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu	
130 135 140	
aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca	480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro	
145 150 155 160	
tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa	528
Tyr Ser Val Gly Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu	
165 170 175	
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Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro	
180 185 190	
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Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr	
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Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu	
210 215 220	
gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att	720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile	
225 230 235 240	
gca atg gcc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac	768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp	
245 250 255	
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Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala	
260 265 270	
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Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu	
275 280 285	
ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc	912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser	
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Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro	
310 315 320	
cgt gcg gat att tct gat ttt gca cgc cgt att tac act atg aaa att	1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile	
325 330 335	
gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att	1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile	

340	345	350	
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atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Ala Gly Ala Val 385 390 395 400			1200
tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser 405 410 415			1248
atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu 420 425 430			1296
gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val 435 440 445			1344
act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr 450 455 460			1392
atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala 465 470 475 480			1440
gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat Asp Val Ala Ala Glu Glu Asn Ala 485			1494
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agcaatttca tcogtggtta aagtgcctgc taattttccc attttgggta tgttgtttaa			1614
cagcttgtgt taatcatgaa caagtttttc ttccaaaaga gaaattaatg ttagcagagc			1674
aacatccgaa tgatcatctt gagcatgagg tgatggttgc gcaaaattagc gaattgttac			1734
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acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaaa ttagcgttgt			1854
atccaaagt ggcagcagcg tttaattatt taggtttata tttattgtta gaggaagatt			1914
acagcgcac tctagatatc tttaatgtgt tgtttgaact tgatccctaa tatgagtatg			1974
cattcctaaa tagagggcta aatttttatt acgtcggacg ttatgaatta gctcagcggg			2034
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<400> 44

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Ile	Thr	Glu	Asn	Lys	His	Val	Met	Asn	Lys	Ile	Asp	Ala	Ile	Lys	Ala
	35					40					45				
Asp	Val	Ile	Ala	Gln	Ile	Thr	Ala	Glu	Val	Ala	Glu	Gly	Glu	Asp	Ile
	50					55					60				
Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu	Glu	Ser	Gln	Ile
65				70					75						80
Val	Arg	Ser	Arg	Ile	Ile	Ala	Gly	Glu	Pro	Arg	Ile	Asp	Gly	Arg	Thr
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Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile	Cys	Thr	Gly	Val	Leu	Pro	Arg
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Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr	Gln	Ala	Leu	Ala
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Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu
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Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro
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Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu
			165					170						175	
Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro
		180						185						190	
Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr
	195						200						205		
Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu
	210					215					220				
Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile
225				230						235				240	
Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp
			245					250						255	
Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala
	260							265					270		
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu
	275						280						285		
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser
	290					295						300			

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro  
305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile  
325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile  
340 345 350

Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp  
355 360 365

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val  
370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val  
385 390 395 400

Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser  
405 410 415

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu  
420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val  
435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr  
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Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala  
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Asp Val Ala Ala Glu Glu Asn Ala  
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<211> 633

<212> DNA

<213> *Pasteurella multocida*

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<222> (2)..(631)

<220>

<223> purF

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ggg gaa aaa att gca cgg gaa tgg gcg gat gtg gat gat att gat gtg 97  
Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val  
20 25 30

gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145  
Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala  
35 40 45

cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193  
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
 50 55 60

gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241  
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser  
 65 70 75 80

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289  
 Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn  
 85 90 95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337  
 Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln  
 100 105 110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385  
 Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala  
 115 120 125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg 433  
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met  
 130 135 140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481  
 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile  
 145 150 155 160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg 529  
 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala  
 165 170 175

tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat 577  
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp  
 180 185 190

tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa 625  
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 195 200 205

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 Tyr Leu  
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 35 40 45

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr  
 50 55 60

Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser  
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Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn  
85 90 95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln  
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Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala  
115 120 125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met  
130 135 140

Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile  
145 150 155 160

Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala  
165 170 175

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp  
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Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu  
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Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile  
20 25 30

act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta 144  
Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu  
35 40 45

aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat 192  
Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp  
50 55 60

ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc 240  
Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser

65	70	75	80
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aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys 100 105 110	336		
cca aaa aac tgc gca gaa aga aaa gaa cga tat tca gaa cag gac att Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Ser Glu Gln Asp Ile 115 120 125	384		
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gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe 165 170 175	528		
ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser 180 185 190	576		
aga gat gtg ccg ctt tgc caa aga gct gtt gcg cta att tta aaa atg Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met 195 200 205	624		
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 tcacacatat catctgcgaa ctcatgagct tctactgcac catctaaca actttgttta 3076  
 gcttgatnta atgtttctgt taagttaacg atatgtatgt cattagatgc atctactgag 3136  
 aaaaattttt tttctgttct tatcatagtt aaatttcctta ttcttttatt aatgggcgag 3196  
 gaatcgggtg ccagtggtga acgttaatag ctatgacata aattggacca ttctgattta 3256  
 tagctaccca aaaatatcca ccatcagcaa tttctcttga tgcaattgcg taatgctcgc 3316  
 catattcacc ttcacaaaaa gcaatgactg gtgtttcaac ttctggtaac ttgtcatcaa 3376  
 cactaatcca gttgctatat tcccaatgaa aattaagctt ctcatagcca ttgatgactt 3436  
 gatctaacgc aggtctttaa tgggtttctc caacaataat atgtgttgtt atcttaactc 3496  
 ctgggattcc atctattact tcacaccagt ttttttcaat aaagtccaat ctttttttat 3556  
 ctgctaaaag actttcatat tctgcttttg tgattgttac tgtttctgtc atagttaaat 3616  
 tcctcatgat aaattccatg tttatttacc ttttttctgg cacaaaaaaa cacgctattg 3676  
 cgtgctgtct tgattgatat aatcaattaa tctaagccca atccatttca taactggaac 3736  
 agccatactg tttccaattg ctttgtatcg tggagaatca gggcattcat ctattgattt 3796  
 gttgcgatat gggattttag tgtaatcgtc tggaaatccc tgtaatcttt cacactcacg 3856  
 cggcgtagt tttctaacaa ctgattctac tgataaagca acgcaaggaa cattattacc 3916  
 accagttccc attctgtgct ttaagggttg tgaatatatca tcgtgaatac gacaagcttc 3976  
 ttcaccctta acctcaata gaatattttc caatcctcca tttcttccaa tgcaatgcgc 4036  
 tgtattttta gaaatgattg gatcttga accgtgaaca acaaaagttt cactaccgcc 4096  
 agcaagaact ccaccgcttg ctcttaatgt tcccgcaaca tcggatttgc gatattgagc 4156  
 aaagcttgct tcaataaagg cggaatatc ttttgctgc gttccgctct gttcaatatt 4216  
 ccctgcgacg cttttggact caatgagtat ttgtgcaaca cttcgtttc tagcacttgc 4276  
 cacaagaaac actcttttac gacgttgggc aactccgaag tattgagcat cgagaactcg 4336  
 ccagcagatt gttcggattg aatgcacata accagcgctc gtccatcttc tccctgtgtg 4396  
 ctgcaatggc tcacactctt gaaccagctc agccagaagg tgcctgaatg cgttgtccga 4456  
 ggtgatagc acacccggaa cgttttccca caggagaatg caggtgtggt tggtgtcatt 4516  
 gaatctaaca tagtgcagc cttctaaaat ttaattaaa actaacgtga gatttctcgc 4576  
 ctcatcgctc aaactttgac gattgccagc aactgaaaaa gattgacaag gagtaccacc 4636  
 aactaaaacg tctgggtgcc gaatttcacg atctaataat ttctgttgca attcagtcac 4696  
 atcaccaaga ttgggaacgt tagggaatg gtaagctaact actgcgcttg ggaattgctc 4756

&lt;210&gt; 48

&lt;211&gt; 292

&lt;212&gt; PRT

<213> *Pasteurella multocida*

&lt;400&gt; 48

Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp  
 1 5 10 15

Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile  
 20 25 30

Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu  
 35 40 45

Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp  
 50 55 60

Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser  
 65 70 75 80

Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile  
 85 90 95

Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys  
 100 105 110

Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile  
 115 120 125

Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile  
 130 135 140

Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr  
 145 150 155 160

Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe  
 165 170 175

Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser  
 180 185 190

Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met  
 195 200 205

Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser  
 210 215 220

Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His  
 225 230 235 240

Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys  
 245 250 255

Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu  
 260 265 270

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala  
 275 280 285

Asn Leu Leu Asp  
290

<210> 49  
<211> 1618  
<212> DNA  
<213> Pasteurella multocida

<220>  
<221> CDS  
<222> (2) ..(1195)

<220>  
<223> sopE

<400> 49  
g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49  
Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile  
1 5 10 15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97  
Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly  
20 25 30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145  
Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
35 40 45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193  
Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly  
50 55 60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241  
Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
65 70 75 80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289  
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
85 90 95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337  
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
100 105 110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385  
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Ile Ala Lys  
115 120 125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433  
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
130 135 140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481  
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
145 150 155 160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529  
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
165 170 175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577

Val	Gln	Tyr	Lys	Arg	Asn	Phe	Ser	Gln	Arg	Glu	Val	Met	Leu	Ile	Met	
			180					185					190			
ggc	gat	ttt	ctg	tca	ttt	aat	gtc	aac	aca	tca	aaa	gtt	gag	att	gac	625
Gly	Asp	Phe	Leu	Ser	Phe	Asn	Val	Asn	Thr	Ser	Lys	Val	Glu	Ile	Asp	
		195				200					205					
tat	gcc	gtc	act	cgt	gcg	gcg	gca	atg	cgt	gca	tat	ctt	gat	aaa	gaa	673
Tyr	Ala	Val	Thr	Arg	Ala	Ala	Ala	Met	Arg	Ala	Tyr	Leu	Asp	Lys	Glu	
	210				215					220						
cag	ggc	tgg	cat	acg	tct	att	tca	aat	aaa	ggc	att	aat	ggc	gtg	agc	721
Gln	Gly	Trp	His	Thr	Ser	Ile	Ser	Asn	Lys	Gly	Ile	Asn	Gly	Val	Ser	
225				230					235				240			
ggg	gtc	aca	caa	cca	ctc	tat	ttt	gac	att	aac	gac	agc	tcg	act	gat	769
Gly	Val	Thr	Gln	Pro	Leu	Tyr	Phe	Asp	Ile	Asn	Asp	Ser	Ser	Thr	Asp	
			245					250					255			
gtg	aac	tat	ctc	aat	gaa	caa	ggc	atc	acg	tgt	tgc	gtg	aat	cat	aat	817
Val	Asn	Tyr	Leu	Asn	Glu	Gln	Gly	Ile	Thr	Cys	Cys	Val	Asn	His	Asn	
			260				265					270				
ggc	ttt	cgt	ttt	tgg	ggc	tta	cgc	acg	act	gca	gaa	gat	cca	tta	ttc	865
Gly	Phe	Arg	Phe	Trp	Gly	Leu	Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe	
		275				280						285				
aag	ttt	gaa	gtg	tac	acc	cgc	act	gca	caa	atc	tta	aaa	gat	acg	att	913
Lys	Phe	Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile	
		290				295					300					
gca	ggg	gcg	ttt	gat	tgg	gca	gtg	gat	aaa	gat	att	tct	gtc	acg	cta	961
Ala	Gly	Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	
	305				310				315					320		
gtg	aaa	gat	att	att	gaa	gca	atc	aat	gcg	aag	tgg	cgt	gat	tac	acc	1009
Val	Lys	Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr	
			325					330						335		
aca	aaa	ggc	tac	tta	att	ggc	ggt	aaa	gcg	tgg	ctt	aat	aaa	gag	ctt	1057
Thr	Lys	Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu	
			340					345					350			
aac	agt	gca	acg	aat	tta	aaa	gat	gcg	aag	ttg	ttg	atc	tct	tat	gat	1105
Asn	Ser	Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp	
			355				360						365			
tat	cac	cca	gta	cca	ccg	ctc	gaa	cag	cta	ggc	ttt	aat	cag	tac	att	1153
Tyr	His	Pro	Val	Pro	Pro	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile		
			370			375							380			
tct	gat	gaa	tac	ctt	gtt	gat	ttt	tca	aat	cgt	tta	gca	tcg			1195
Ser	Asp	Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser			
			385			390				395						
taaggggtag	aaaatggctt	taccacgcaa	acttaaatg	atgaatttaa	tcacgcagcg											1255
taacaaatat	ctcgcggaag	tcacggaagt	gactcaacca	aaattagcaa	tgaaaatcga											1315
agaatttcgc	gcggcgcgga	tgattggttc	ggtgatgtc	aatctcgggc	ttgaaaagct											1375
cgaagcgga	tttaaagccg	gtggctacat	ggtcgaatta	attaaaaaat	tcggcggttc											1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495  
 cacatctgtt gagcttgtga tgcaaggctg atttactgaa attgacagcg gaaacagcaa 1555  
 agtgggcat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615  
 tga 1618

<210> 50  
 <211> 398  
 <212> PRT  
 <213> Pasteurella multocida

<400> 50  
 Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile  
 1 5 10 15  
 Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly  
 20 25 30  
 Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn  
 35 40 45  
 Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly  
 50 55 60  
 Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val  
 65 70 75 80  
 Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp  
 85 90 95  
 Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile  
 100 105 110  
 Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys  
 115 120 125  
 Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp  
 130 135 140  
 Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn  
 145 150 155 160  
 Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala  
 165 170 175  
 Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met  
 180 185 190  
 Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp  
 195 200 205  
 Tyr Ala Val Thr Arg Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu  
 210 215 220  
 Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser  
 225 230 235 240  
 Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp  
 245 250 255

Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn  
260 265 270

Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe  
275 280 285

Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile  
290 295 300

Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu  
305 310 315 320

Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr  
325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu  
340 345 350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp  
355 360 365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile  
370 375 380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
385 390 395

<210> 51

<211> 353

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1)..(351)

<220>

<223> unknown C1

<400> 51

atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat 48  
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn  
1 5 10 15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96  
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe  
20 25 30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144  
Tyr Phe Leu Glu Lys Lys Glu Phe Asn Phe Gln Asp Tyr Ser Phe  
35 40 45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192  
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys  
50 55 60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240  
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile  
65 70 75 80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu  
85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336  
Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg  
100 105 110

gtc atc tat aaa aga ta 353  
Val Ile Tyr Lys Arg  
115

<210> 52

<211> 117

<212> PRT

<213> *Pasteurella multocida*

<400> 52

Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn  
1 5 10 15

Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe  
20 25 30

Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe  
35 40 45

Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys  
50 55 60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile  
65 70 75 80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu  
85 90 95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg  
100 105 110

Val Ile Tyr Lys Arg  
115

<210> 53

<211> 509

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1) .. (507)

<220>

<223> unknown C2

<400> 53

atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48  
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val  
1 5 10 15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96  
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu

20 25 30  
 cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144  
 Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser  
 35 40 45  
 gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192  
 Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe  
 50 55 60  
 tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240  
 Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Glu Ser Ala Ser  
 65 70 75 80  
 cct gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288  
 Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly  
 85 90 95  
 tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336  
 Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile  
 100 105 110  
 tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384  
 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
 115 120 125  
 atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432  
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu  
 130 135 140  
 ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480  
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser  
 145 150 155 160  
 ttt gat gaa atg ata gag aag tat tcg ta 509  
 Phe Asp Glu Met Ile Glu Lys Tyr Ser  
 165  
 <210> 54  
 <211> 169  
 <212> PRT  
 <213> *Pasteurella multocida*  
 <400> 54  
 Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val  
 1 5 10 15  
 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu  
 20 25 30  
 Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser  
 35 40 45  
 Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe  
 50 55 60  
 Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser  
 65 70 75 80  
 Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly  
 85 90 95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile  
 100 105 110  
 Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys  
 115 120 125  
 Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu  
 130 135 140  
 Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser  
 145 150 155 160  
 Phe Asp Glu Met Ile Glu Lys Tyr Ser  
 165

<210> 55  
 <211> 443  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1) .. (441)

<220>  
 <223> unknown C3

<400> 55  
 atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta 48  
 Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu  
 1 5 10 15  
 ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt 96  
 Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val  
 20 25 30  
 tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag 144  
 Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu  
 35 40 45  
 ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga 192  
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg  
 50 55 60  
 ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag 240  
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu  
 65 70 75 80  
 gtt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat 288  
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp  
 85 90 95  
 ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag 336  
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu  
 100 105 110  
 cca aat ttt aaa ggt agt gcc tgg gta aga tat tct tat aat gga aga 384  
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg  
 115 120 125  
 aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc 432

Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser  
130 135 140

att ttt att ta  
Ile Phe Ile  
145

443

<210> 56  
<211> 147  
<212> PRT  
<213> *Pasteurella multocida*

<400> 56  
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu  
1 5 10 15

Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val  
20 25 30

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu  
35 40 45

Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg  
50 55 60

Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu  
65 70 75 80

Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp  
85 90 95

Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu  
100 105 110

Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg  
115 120 125

Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser  
130 135 140

Ile Phe Ile  
145

<210> 57  
<211> 8498  
<212> DNA  
<213> *Pasteurella multocida*

<220>  
<223> unknown C

<400> 57  
gaattcgaat taagcgagaa aattgctgaa acactagaac aaagtcaatt aaatattagt 60  
caattatcaa ttgttgaaat ttatcctttc atgaagaac aagggatacg ttttcataat 120  
aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcttttc 180  
tttgtggcg atattcagca agtcgctcat ctgcgaaaag ccgcagaaat gggttgcgtg 240

gtgattgata tgaagggat ttgtgccagc tgcaagacg tccctgtggt gataccggga 300  
 gtaaatcagg aaaaattggt agatttacgt cagcgtaata ttgtgtcctt agccgatcca 360  
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Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly Asn Ile Gly Arg	
405 410 415 420	
aga aca act cga gct tgg ttt gat caa aaa aat aaa gat att aca aga	3993
Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys Asp Ile Thr Arg	
425 430 435	
gag ttg aat att gtt cgt cct tct ggt tgg act tct gca tct tgg ggg	4041
Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser Ala Ser Ser Gly	
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ctt ctt gtt gga gct aat atc atg atg gag gag aat aag aat cct gat	4089
Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn Lys Asn Pro Asp	

455

460

465

gcg caa cct tcg aaa ctc ggg aca aat att caa cgt gtt atc tta gta 4137  
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tta tct gat ggt gaa gat aac tgg cca act tat agt aca tta acg act 4185  
 Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser Thr Leu Thr Thr  
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ctt tta aac aat ggt atg tgt gac aaa att cga gaa caa ttg ggc aag 4233  
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gcg ttt ggc tat agt cca cca gca aac caa gtt gcc gct tgg aaa aaa 4329  
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gat agt ttc aaa caa att att gga ttt gaa gaa gag gtg ggg cgt tct 4425  
 Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Val Gly Arg Ser  
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tca tct cat aaa ccg aaa ttt taagattgtc caaggataac gctaaaaaat 4476  
 Ser Ser His Lys Pro Lys Phe  
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ttaattcatt acataacata actttttcgt gaataatata gaataagacaa caataagaat 4596

taaaacgctc aaggcataga ggcttagtcg aacaaactaa gctattttgc gcgattgatt 4656

gggatataga tgttatttca aataagcaat aaccatggta ctgagaaaga agatgagtgc 4716

cgtaataaag tagaagcgat ttttcttttg gctgaaaggt ggtgttatgcc ttttctggct 4776

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5798

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 Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala  
 50 55 60  
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 Gly Asp Val Asn Arg Gln Val Val Ser Pro Gln Asp Lys Ala Lys Phe  
 85 90 95  
 Gly Gly Asn Glu Phe Met Ala Lys Gln Glu Lys Arg Asn Gln Glu Leu  
 100 105 110  
 Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala  
 115 120 125  
 Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys  
 130 135 140  
 Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro  
 145 150 155 160  
 Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro  
 165 170 175  
 Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val  
 180 185 190  
 Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val

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Ser His Leu Gln Asp Lys Asn Gly Arg Ser Leu Gly Lys Ala Lys Ile 225 230 235 240		
Thr Ile Leu Arg Glu Val Val Ser Glu Ile Ser Lys Ile Leu Leu Pro 245 250 255		
Glu Asp Val Ser Glu Gly Val Ser Pro Phe Asn Arg Ile Gly Phe Thr 260 265 270		
Thr Phe Ser Gly Gly Val Arg Gln Arg Asp Val Thr Gly Cys Val 275 280 285		
Leu Pro Tyr Glu Gly Lys Ile Ser Gln Thr Ser Arg Lys Leu Thr Ile 290 295 300		
Arg Tyr Trp Ile Thr Gly Asn Asn Thr Pro Trp Lys Phe Asn Ala Gly 305 310 315 320		
Arg Trp Glu Arg Ser Thr Val Ser Phe Gln Glu His Tyr Lys Gly Tyr 325 330 335		
Tyr Asp Lys Phe His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg 340 345 350		
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Lys Ile Asn Asp Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile 370 375 380		
Asp Val Ser Gly Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn 385 390 395 400		
Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly 405 410 415		
Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys 420 425 430		
Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser 435 440 445		
Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn 450 455 460		
Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg 465 470 475 480		
Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser 485 490 495		
Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu 500 505 510		
Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg 515 520 525		

Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala  
530 535 540

Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys  
545 550 555 560

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565 570 575

Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe  
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gtaaatgttc aaacagggat tagtattgat gcggctttaa aacaagtggc aatcgatttt 360

aagaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420

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acattatcag ctaaaatgag tatccattg attttgttta ttatgttccc aataatcatt 660

ttaattctag caccaggtat aatgagggta ttcccaa atg ttt ttt aaa ttt acc 715

Met Phe Phe Lys Phe Thr

1

5

aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct 763

Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser

10

15

20

acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811

Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr

25

30

35

ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca 859

Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala

40	ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca	907
	Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser	
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	ata cgc tat aaa tta cgc aag aca tac tat cag cga ggt gac agc aaa	955
	Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys	
	75 80 85	
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	Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu	
	90 95 100	
	gct aca caa cgc aaa ata tta cag ata aaa aat cta att caa tta aat	1051
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	Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Lys Ser	
	120 125 130	
	cct aat gaa gga gaa gta tat aat tta aga ggt atc gct tat cgc caa	1147
	Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln	
	135 140 145 150	
	aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag	1195
	Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu	
	155 160 165	
	ttc ttt att aat gat aat gtt gct att aat aat tta gcc atg cta aat	1243
	Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn	
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	att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa	1291
	Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Leu Pro Gln	
	185 190 195	
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	Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe	
	200 205 210	
	gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt	1387
	Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val	
	215 220 225 230	
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	Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys	
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	aaa act aca cat gta tca aaa ggt gta act cgg taactactaag gatttgatat	1488
	Lys Thr Thr His Val Ser Lys Gly Val Thr Arg	
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 35 40 45  
 Thr Gln Asn Tyr Ser Ala Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys  
 50 55 60  
 Ala Lys Glu Asp Pro Ser Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr  
 65 70 75 80  
 Gln Arg Gly Asp Ser Lys Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu  
 85 90 95  
 Asn Asp Asn Thr Lys Leu Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys  
 100 105 110  
 Asn Leu Ile Gln Leu Asn Asn Phe Gln Glu Ala Ile Ser Val Ala Asn  
 115 120 125  
 Glu Leu Leu Leu Lys Ser Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg  
 130 135 140  
 Gly Ile Ala Tyr Ala Gln Asn Gly Asn Leu Val Asn Ala Arg Asn Asp  
 145 150 155 160  
 Ile Asn Lys Ala Arg Glu Phe Phe Ile Asn Asp Asn Val Ala Ile Asn  
 165 170 175  
 Asn Leu Ala Met Leu Asn Ile Ile Asn Gly Asp Phe Asn Asn Ala Val  
 180 185 190  
 Ser Leu Leu Leu Pro Gln Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu  
 195 200 205  
 Ile His Asn Leu Val Phe Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr  
 210 215 220  
 Ala Lys Asp Ile Ile Val Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp

225

230

235

240

Leu Ile Asn Ala Leu Lys Lys Thr Thr His Val Ser Lys Gly Val Thr  
 245 250 255

Arg

&lt;210&gt; 62

&lt;211&gt; 1788

&lt;212&gt; DNA

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&lt;220&gt;

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&lt;220&gt;

&lt;223&gt; unknown K

&lt;400&gt; 62

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 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
 20 25 30

aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144  
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
 35 40 45

aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt 192  
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
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 65 70 75 80

acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288  
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly  
 85 90 95

aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat 336  
 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Tyr  
 100 105 110

ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac 384  
 Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn  
 115 120 125

ctc aca gcg gat cgc acg gtg tac aat tta ggg aat att ttt gct aaa 432  
 Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys  
 130 135 140

ggg gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc 480  
 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu  
 145 150 155 160

aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat 528  
 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Asp Tyr Thr Arg Tyr  
 165 170 175

tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat 576  
 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr  
 180 185 190

gaa tta aac gtc gac aga gtt tct tgatttgtgc atcaattttg taaccaccgg 630  
 Glu Leu Asn Val Asp Arg Val Ser  
 195 200

ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgt gcgacgatca 690  
 catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat 750  
 tgggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgcttt 810  
 catgaataat ggcagcacct aaatgttttg ctaaatcaat ggcacgagtc gcaattaat 870  
 ctgcgctcca aggaatacat gccagattt taattgggct tttctcaaat aatgataaaa 930  
 tctcagatgc ttgattttgt gtgtgttgga aagaatcaaa aatttctgcc aagtcagggc 990  
 gagtacgacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaaat 1050  
 tagggttatt ttgtctgcca aataatgagg ctgcggcttt gatgcgttct ttgagttctg 1110  
 ccggtgtttc cgtgcgggt gctgcaacaa gaatgatttc cgcatacagt gcttgagcaa 1170  
 ttcatagatt aatgctattg gcataagaat gcttacgcgt agggattaaa ccttccacca 1230  
 cgacaatttc attgtttttg gcgagttgtt gatgattttc aacaattttt tctagtacca 1290  
 catcagattg attttgaccg atgagtgatt cagctacact taacataaat gggtcactgg 1350  
 ttccaatggt ggtactgggt cgaataattg atgttgtgcg atcaatcata tcttcacctg 1410  
 agttcggctg agaaattggt ttcataaagc cgactttcgc ccttttttgc tccagtgcac 1470  
 gtgttaaacc taagctgaca ctggttaagc ctacaccagc actaatcggg ataaggataa 1530  
 ttgtactgta cataataaac cctaatttgt tgataattta tacaaaaaga aactgccgat 1590  
 gaatcggcag ttaattgatc tttagcgcat gcaaaggcgc gcggatattt gtgcaataac 1650  
 aagttcttca ttctgtggga tcaccatggc aacaggcgta ttgtctgctg taatcaccoc 1710  
 ttcatgacca aagcgagccg cttgtttttt atctgaatcc acttgataac cgaacagttt 1770  
 taaatggttt aaggttga 1788

<210> 63  
 <211> 200  
 <212> PRT  
 <213> Pasteurella multocida

<400> 63  
 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe  
 1 5 10 15

Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala  
20 25 30

Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala  
35 40 45

Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly  
50 55 60

Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn  
65 70 75 80

Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly  
85 90 95

Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr  
100 105 110

Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn  
115 120 125

Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys  
130 135 140

Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu  
145 150 155 160

Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr  
165 170 175

Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr  
180 185 190

Glu Leu Asn Val Asp Arg Val Ser  
195 200

<210> 64

<211> 278

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (108)..(278)

<220>

<223> unknown O

<400> 64

gaattccaac caaatctcac accagagcaa gaacgtacata tagtgggaatg gttggcagaa 60

cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116  
Met Lys Ile  
1

act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164  
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu  
5 10 15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212  
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu

20 25 30 35

gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260  
 Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu  
 40 45 50

agc aaa agg gga cat agt 278  
 Ser Lys Arg Gly His Ser  
 55

<210> 65  
 <211> 57  
 <212> PRT  
 <213> Pasteurella multocida

<400> 65  
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
 1 5 10 15  
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
 20 25 30  
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
 35 40 45  
 Glu Glu Glu Ser Lys Arg Gly His Ser  
 50 55

<210> 66  
 <211> 1020  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1)..(597)  
 <220>  
 <223> unknown P

<400> 66  
 gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg 48  
 Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala  
 1 5 10 15  
 gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96  
 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile  
 20 25 30  
 tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144  
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr  
 35 40 45  
 ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192  
 Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln  
 50 55 60  
 ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240  
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu  
 65 70 75 80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288  
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg  
 85 90 95  
 act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca 336  
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala  
 100 105 110  
 gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384  
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala  
 115 120 125  
 atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432  
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly  
 130 135 140  
 ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480  
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys  
 145 150 155 160  
 gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528  
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu  
 165 170 175  
 gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576  
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp  
 180 185 190  
 ttt tca aat cgt tta gca tgg taaggggtag aaaatggcctt taccacgcaa 627  
 Phe Ser Asn Arg Leu Ala Ser  
 195  
 acctaaaattg atgaatttaa tcatcgacgg taacaaatat ctgcgcgaag tcacggaagt 687  
 gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc 747  
 ggtggatgac aatctcgggc ttgaaaagct cgaagcggaa tttaagccg gtggctacat 807  
 ggtcgaatta attaaaaaat tcggcgggac aatcaacggc attccattgc gttttcttgg 867  
 ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttctga tgcaaggtcg 927  
 atttactgaa attgacagcg gaaacagcaa agtgggagat gacactgaac aaacattcaa 987  
 agtgccttta acgtattaca aaatcattgt tga 1020

<210> 67  
 <211> 199  
 <212> PRT  
 <213> *Pasteurella multocida*

<400> 67  
 Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala  
 1 5 10 15  
 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile  
 20 25 30  
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr  
 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln  
 50 55 60  
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu  
 65 70 75 80  
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg  
 85 90 95  
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala  
 100 105 110  
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala  
 115 120 125  
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly  
 130 135 140  
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys  
 145 150 155 160  
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu  
 165 170 175  
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp  
 180 185 190  
 Phe Ser Asn Arg Leu Ala Ser  
 195

<210> 68  
 <211> 2584  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (1042)..(2286)

<220>  
 <223> xyla

<400> 68  
 gtcgaccagc ttagattttg cgacgggggt aattttttct atcgtttcaa tcattgcggt 60  
 taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120  
 cgcgatggtc tttttggtct ttatttacgt gctgttttagc agtattgtgg catttaaaat 180  
 cggtcgccgc ttaattcagc tcaattttgc caatgaacgc ttaaacgccca actaccgtta 240  
 ttcacttata cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300  
 ggaaaaacgt ctattgacca cacaatttaa tcagggtgatt gataacggtt ggcaagtaat 360  
 ctaccgcacc ttgaaattat cgggttttaa cttaatcatt acgcagattt cgggtggttt 420  
 tccgtggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtggt 480  
 agaatacgca tacttttctg tggaaaagta aactctttaa tataaataga aatcgcttga 540



175	180	185	
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu 190 195 200			1647
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Val Val Glu 205 210 215			1695
cat .aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys 220 225 230			1743
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val 235 240 245 250			1791
tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn 255 260 265			1839
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu 270 275 280			1887
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn 285 290 295			1935
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser 300 305 310			1983
gta gaa gaa aat act ttg gtc ata tat gaa att ctg aaa gca ggg ggc Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly 315 320 325 330			2031
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser 335 340 345			2079
acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val 350 355 360			2127
ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala 365 370 375			2175
tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu 380 385 390			2223
ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg 395 400 405 410			2271
cta aca aaa gtg ctt taaaacgttc cggttacgc cagacatcta gacgattgaa Leu Thr Lys Val Leu 415			2326

taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386  
 acaacaaagt tctgcacaaat cttgaattgc gtgaggaat ttaaagcgct gacataagcg 2446  
 tcttgtcggc atgacaccag ctttttcatg tccataatga tgtgggaata tttcttttgg 2506  
 tgtaaggct tttcctaata catgacaaat tgcagcaaaa cgtaccgcac ttttgtcaact 2566  
 gtccgtgttt tctgtcga 2584

<210> 69  
 <211> 415  
 <212> PRT  
 <213> Pasteurella multocida

<400> 69  
 Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val  
 1 5 10 15  
 Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val  
 20 25 30  
 Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr  
 35 40 45  
 Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser  
 50 55 60  
 Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys  
 65 70 75 80  
 Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro  
 85 90 95  
 Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe  
 100 105 110  
 Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln  
 115 120 125  
 Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys  
 130 135 140  
 Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro  
 145 150 155 160  
 Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala  
 165 170 175  
 Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu  
 180 185 190  
 Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln  
 195 200 205  
 Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly  
 210 215 220  
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys  
 225 230 235 240

His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln  
 245 250 255  
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala  
 260 265 270  
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala  
 275 280 285  
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu  
 290 295 300  
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu  
 305 310 315 320  
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe  
 325 330 335  
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu  
 340 345 350  
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys  
 355 360 365  
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn  
 370 375 380  
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile  
 385 390 395 400  
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu  
 405 410 415

<210> 70  
 <211> 3501  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (298) .. (1905)

<220>  
 <223> yabk

<400> 70  
 gaattcgagg aagggggcgt attacaaatt gaaacggctg cactgttagc acaacatgat 60  
 aatgcctgtg cggatcattt ccttgccttt ttacttcac cagaagcaca agggcattta 120  
 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180  
 cttagagcca cccaaatgaa cagcaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240  
 gtcaaaaaat ggattgtgtg ttggcaaacg accctaacc aataattggt tgtcttg 297  
 atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345  
 Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu  
 1 5 10 15  
 ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc 393

Gly	Gly	Met	Leu	Val	Ile	Val	Phe	Leu	Ser	Ala	Phe	Tyr	Ala	Phe	Ala		
			20					25					30				
tta	ggg	gcg	gtt	ttt	tcg	ctc	cct	ttt	gcg	cgc	agt	tgg	aca	gcg	tgg	441	
Leu	Gly	Ala	Val	Phe	Ser	Leu	Pro	Phe	Ala	Arg	Ser	Trp	Thr	Ala	Leu		
		35					40					45					
ttg	agt	gat	cag	tat	tta	caa	cac	gtg	atc	atc	ttt	agc	ttt	tgg	caa	489	
Leu	Ser	Asp	Gln	Tyr	Leu	Gln	His	Val	Ile	Ile	Phe	Ser	Phe	Trp	Gln		
	50					55					60						
gcc	ttt	ctg	tcg	gcg	gta	ctt	gcg	gtc	ctc	ttt	ggc	ggc	att	gta	gca	537	
Ala	Phe	Leu	Ser	Ala	Val	Leu	Ala	Val	Leu	Phe	Gly	Gly	Ile	Val	Ala		
	65				70					75					80		
cga	gcc	ttt	ttt	tat	caa	ccg	ttt	gtg	ggc	aag	aaa	ctg	atc	ctc	aaa	585	
Arg	Ala	Phe	Phe	Tyr	Gln	Pro	Phe	Val	Gly	Lys	Lys	Leu	Ile	Leu	Lys		
			85						90					95			
tta	ttt	tca	ctg	act	ttt	gtg	tta	cct	gcc	tta	gtg	gcg	att	ttt	ggc	633	
Leu	Phe	Ser	Leu	Thr	Phe	Val	Leu	Pro	Ala	Leu	Val	Ala	Ile	Phe	Gly		
			100					105					110				
tta	tta	ggc	gtg	tat	ggc	gct	tct	ggc	tgg	tta	gcg	atg	tta	agc	cag	681	
Leu	Leu	Gly	Val	Tyr	Gly	Ala	Ser	Gly	Trp	Leu	Ala	Met	Leu	Ser	Gln		
		115					120					125					
ttt	ttc	gct	tgg	gat	tgg	act	cct	aat	att	tac	ggc	tta	aca	ggc	att	729	
Phe	Phe	Ala	Trp	Asp	Trp	Thr	Pro	Asn	Ile	Tyr	Gly	Leu	Thr	Gly	Ile		
		130				135					140						
tta	ctg	gcg	cat	ctt	ttt	ttt	aat	gtc	cca	tta	gct	tgt	cgc	ctg	ttt	777	
Leu	Leu	Ala	His	Leu	Phe	Phe	Asn	Val	Pro	Leu	Ala	Cys	Arg	Leu	Phe		
		145			150				155					160			
tta	caa	ggc	ttg	caa	gca	att	ccg	gtg	caa	caa	cgt	cag	ctc	gcg	gca	825	
Leu	Gln	Gly	Leu	Gln	Ala	Ile	Pro	Val	Gln	Gln	Arg	Gln	Leu	Ala	Ala		
			165					170						175			
caa	ctc	aat	tta	cgt	ggc	tgg	cat	ttt	ata	cgt	ctg	att	gag	tgg	ccc	873	
Gln	Leu	Asn	Leu	Arg	Gly	Trp	His	Phe	Ile	Arg	Leu	Ile	Glu	Trp	Pro		
			180				185						190				
tat	tta	cgc	cag	caa	ttg	tta	cct	gca	ttt	act	ttg	att	ttc	atg	ctg	921	
Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu		
		195					200					205					
tgt	ttt	acc	agt	ttt	gcg	att	gtg	ctc	act	tta	ggc	ggc	gga	ccg	aaa	969	
Cys	Phe	Thr	Ser	Phe	Ala	Ile	Val	Leu	Thr	Leu	Gly	Gly	Gly	Pro	Lys		
		210				215					220						
tat	acc	acg	ttg	gaa	gtg	gct	atc	tat	caa	gcg	att	tta	ttt	gag	ttt	1017	
Tyr	Thr	Thr	Leu	Glu	Val	Ala	Ile	Tyr	Gln	Ala	Ile	Leu	Phe	Glu	Phe		
		225			230				235					240			
gat	gta	ccg	aaa	gcc	ggc	tta	ttt	gcg	tta	tta	caa	ttt	ggt	ttt	tgt	1065	
Asp	Val	Pro	Lys	Ala	Gly	Leu	Phe	Ala	Leu	Leu	Gln	Phe	Val	Phe	Cys		
				245					250					255			
ttt	ctg	tta	ttc	acg	ctg	agt	agc	ttt	ttt	tct	cca	gcc	ccc	gcc	acg	1113	
Phe	Leu	Leu	Phe	Thr	Leu	Ser	Ser	Phe	Phe	Ser	Pro	Ala	Pro	Ala	Thr		
			260					265					270				

aca tta cac agt caa cct act tgg ttt gcg ccc caa tgc tat tgg gtt	1161
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
275 280 285	
aaa tta tgg caa cgt atg att tgg tgt gcg aca gta ttt atc tta	1209
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
290 295 300	
tta ccg cta ctc aat acg cta gtt tct gct ttg ctt tgc tct cag ttt	1257
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Ser Ser Gln Phe	
305 310 315 320	
ttt acc ttg tgg tta caa cct caa tta tgg aaa gca tta ggt tac tgc	1305
Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
325 330 335	
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt	1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Val Leu Ser Phe	
340 345 350	
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca	1449
Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
385 390 395 400	
ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta	1545
Phe Ser Pro Tyr His Leu Phe Gly Val Val Cys Cys Asn Ala Leu	
405 410 415	
gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
420 425 430	
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Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
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Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
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Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
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Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
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Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
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gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa	1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu	

cga cat cag gaa cgg cgt gat gat taatttaaac ggtgttcagt ttctctataa 1935  
 Arg His Gln Glu Pro Arg Asp Asp  
 530 535

tacctttact tttagctggt atttgcatat tctgtctcaa caaaaagtty ctattattgg 1995  
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Leu	Ser	Asp	Gln	Tyr	Leu	Gln	His	Val	Ile	Ile	Phe	Ser	Phe	Trp	Gln
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Ala	Phe	Leu	Ser	Ala	Val	Leu	Ala	Val	Leu	Phe	Gly	Gly	Ile	Val	Ala
	65				70					75					80
Arg	Ala	Phe	Phe	Tyr	Gln	Pro	Phe	Val	Gly	Lys	Lys	Leu	Ile	Leu	Lys
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Leu	Leu	Gly	Val	Tyr	Gly	Ala	Ser	Gly	Trp	Leu	Ala	Met	Leu	Ser	Gln
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Phe	Phe	Ala	Trp	Asp	Trp	Thr	Pro	Asn	Ile	Tyr	Gly	Leu	Thr	Gly	Ile
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Leu	Gln	Gly	Leu	Gln	Ala	Ile	Pro	Val	Gln	Gln	Arg	Gln	Leu	Ala	Ala
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Gln	Leu	Asn	Leu	Arg	Gly	Trp	His	Phe	Ile	Arg	Leu	Ile	Glu	Trp	Pro
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Tyr	Leu	Arg	Gln	Gln	Leu	Leu	Pro	Ala	Phe	Thr	Leu	Ile	Phe	Met	Leu
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Phe	Leu	Leu	Phe	Thr	Leu	Ser	Ser	Phe	Phe	Ser	Pro	Ala	Pro	Ala	Thr
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Thr	Leu	His	Ser	Gln	Pro	Thr	Trp	Phe	Ala	Pro	Gln	Ser	Tyr	Trp	Val
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Lys	Leu	Trp	Gln	Arg	Met	Ile	Ile	Val	Cys	Ala	Thr	Val	Phe	Ile	Leu
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Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe  
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Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser  
325 330 335

Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe  
340 345 350

Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser  
355 360 365

Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro  
370 375 380

Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp  
385 390 395 400

Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu  
405 410 415

Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn  
420 425 430

Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly  
435 440 445

Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met  
450 455 460

Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr  
465 470 475 480

Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu  
485 490 495

Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr  
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Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu  
515 520 525

Arg His Gln Glu Pro Arg Asp Asp  
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gctttctcgt	gttcgaaata	aaattattga	tggagcgggt	gcacacgcgg	caatgtatgc	300
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Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile						
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Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr						
25 30 35						
ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca						1699
Leu Ile Ile Phe Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro						
40 45 50						

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ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala 165 170 175 180	2083
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cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile 265 270 275	2371
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295

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305

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 345 350 355

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 Ile Ile Ile Met Met Val Ile Leu Leu Ile Thr Gly Met Phe Leu Asp  
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 375 380 385

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tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt 2803  
 Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly  
 405 410 415 420

act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca ttgctccgt 2859  
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&lt;210&gt; 73

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&lt;212&gt; PRT

&lt;213&gt; Pasteurella multocida

&lt;400&gt; 73

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Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe  
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Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile

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		370				375					380																			

Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile  
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Val Gly Arg Gly Thr Phe  
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<400> 74

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40 45 50

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70 75 80

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Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile  
 85 90 95 100  
 cct tca ata cgt aac ccg gca gca cca ccg ata acg gat gct tgc gcc 810  
 Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala  
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 atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc 858  
 Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly  
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 tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga 906  
 Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly  
 135 140 145  
 tgt gat agt ttt gac ata tta act cca gtc taaatttatc aaaagaagat 956  
 Cys Asp Ser Phe Asp Ile Leu Thr Pro Val  
 150 155  
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<211> 158

<212> PRT

<213> Pasteurella multocida

<400> 75

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Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val  
 35 40 45

Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met  
 50 55 60

Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg  
 65 70 75 80

Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe  
 85 90 95

Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr  
 100 105 110

Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro  
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Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser  
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Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val  
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<210> 76

<211> 2787

<212> DNA

<213> Pasteurella multocida

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<220>  
<223> yiaO

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Met Lys Phe Lys Lys Leu Leu Leu																	
1 5																	
gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac																	2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr																	
10 15 20																	
gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa																	2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys																	
25 30 35 40																	
gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat gcc aaa																	2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys																	
45 50 55																	
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60 65 70																	
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Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu																	
75 80 85																	
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Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu																	
90 95 100																	
cct tat atg att oct aat att gaa acc tct aaa gcg ttg ctc gac																	2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp																	
105 110 115 120																	
aca aaa ttt ggt caa ggt gtt tta tta aaa aaa att gat aaa gag tta aac																	2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn																	
125 130 135																	
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Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser																	
140 145 150																	
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155 160 165																	
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Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala																	
170 175 180																	
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Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr																	
185 190 195 200																	
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Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Leu Ile Gln Ala Gln																	

205										210										215										
aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta	2644																													
Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu																														
220	225	230																												
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Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro																														
235	240	245																												
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Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Lys Ala Ala Glu																														
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tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt	2787																													
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<210> 77

<211> 279

<212> FRT

<213> Pasteurella multocida

<400> 77

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Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu			
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Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser			
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Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly			
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Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe			
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Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu			
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Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu			
115	120	125	
Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr			
130	135	140	
Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu			
145	150	155	160
Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu			
165	170	175	
Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser			
180	185	190	
Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn			

195

200

205

Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr  
210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser  
225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys  
245 250 255

Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp  
260 265 270

Gly Glu Asn Ser Leu Val Glu  
275

&lt;210&gt; 78

&lt;211&gt; 2590

&lt;212&gt; DNA

<213> *Pasteurella multocida*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (908)..(1294)

&lt;220&gt;

&lt;223&gt; yigF

&lt;400&gt; 78

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Gly	Pro	Tyr	Val	Gln	Ala	Val	Asp	Leu	Gly	Asn	Met	Leu	Leu	Thr	Ser	
15				20					25					30		
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Gly	Gln	Ile	Pro	Val	Asn	Pro	Lys	Thr	Gly	Glu	Val	Pro	Ala	Asp	Ile	
				35					40					45		
gta	gca	caa	gca	cgt	caa	tcg	tta	gaa	aac	gtg	aaa	gcg	att	gtg	gaa	1093
Val	Ala	Gln	Ala	Arg	Gln	Ser	Leu	Glu	Asn	Val	Lys	Ala	Ile	Val	Glu	
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Gln	Ala	Gly	Leu	Gln	Val	Ala	Asn	Ile	Val	Lys	Thr	Thr	Val	Phe	Val	
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Lys	Asp	Leu	Asn	Asp	Phe	Ala	Ala	Val	Asn	Ala	Glu	Tyr	Glu	Arg	Phe	
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Phe	Lys	Glu	Asn	Asn	His	Pro	Ser	Phe	Pro	Ala	Arg	Ser	Cys	Val	Glu	
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Val	Ala	Arg	Leu	Pro	Lys	Asp	Val	Gly	Ile	Glu	Ile	Glu	Ala	Ile	Ala	
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Val	Lys	Ala														
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 <212> PRT  
 <213> Pasteurella multocida

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 Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile Val Ala  
 35 40 45  
 Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu Gln Ala  
 50 55 60  
 Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val Lys Asp  
 65 70 75 80  
 Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys  
 85 90 95  
 Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu Val Ala  
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<210> 80  
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 <222> (463) .. (1884)

<220>  
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<400> 80

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gtcagtcaca tttttatagg ttaactgaat tttttaaacg at atg acg caa aaa 474  
Met Thr Gln Lys  
1  
tta cat att aaa acg tgg ggt tgt cag atg aat gaa tat gat tca tct 522  
Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn 15 Glu Tyr Asp Ser Ser 20  
5 10  
aaa atg gca gat ctc tta aac agt act cac ggc tta gag tta aca gaa 570  
Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu 35  
25 30  
att ccg gaa gaa gcg gat gtg tta ttg tta aac act tgc tca att cgt 618  
Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg 50  
40 45  
gaa aaa gca caa gaa aaa gtt ttc cat caa tta gga cgt tgg aaa gaa 666  
Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu 65  
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Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val 80  
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Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala		
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Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr		
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Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly		
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Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly		
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Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu		
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Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His		
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Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro		
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Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg		
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Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser		
275	280	285
Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser		
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Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln		
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Thr Met Asn Leu Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe		
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Ile Tyr Ser Ala Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp		
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Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg		
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Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu  
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Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro  
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 gatcctcatt atcctccctt gttaaagcaa acagaagagg caccacttgt cttggtttgtg 3526  
 aaaggggaag tgggtacgct atctgcacag caagtggcga tcgtgggcag tcgtcattgt 3586  
 tcacgttatg gggaatactg ggcaaatatt ttcgccactc aactggctta tgcgatatt 3646  
 gtggtgacca gtggtttagc gttaggtatt gatgggttct cacatcaagc ggtagtggat 3706  
 atccacggga agacgattgc agtattaggc agtgggttag aggtcattta tccgaaaaaa 3766  
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 tctttgggga cattagtcatt tgaagcctca gaaaacagtg gttctttaat tactgcccgc 3946  
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 agccaagggt gtcataaact gattaaacag ggggcaatat tagtcgaaag tattcaggat 4066  
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 aacgcctttt ctcaacaagt aacagacaca tcaaccatca atactgcgcg gataacgcc 4186  
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 gacttgattg ttgctgaaaa tggattatat cagcgcgaat aacggaaaaga gtaaccacaa 4366  
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 atgacacgag acggcagttt catgagatta atagagacta aacgcttgta aatacggtag 4486  
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 tagctcaata ttgataccaa tacttttgtc ataaaaaatt tgattccgcg ttggtttttc 4606  
 tttgtgggtc acactacgct gggcaccaac attaatcgcc caacagcaag tgctgtattc 4666  
 tagtcccaaa tattgtctca caggctttct caacgcaaga tcttgataat gacgtgtctac 4726  
 caccgcccat tgatccgtga gtgccatgc cacagttaga ccaagctgtt ttatgtcttg 4786  
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<210> 83

<211> 250

<212> PRT

<213> *Pasteurella multocida*

<400> 83

Met Lys Lys Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu  
 1 5 10 15

Ala Thr Arg Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Gly  
 20 25 30

Leu Gln Gln Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro  
 35 40 45  
 Pro Phe Ala Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg  
 50 55 60  
 Cys Gly Gln Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala  
 65 70 75 80  
 Ser Leu Ile Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg  
 85 90 95  
 Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys  
 100 105 110  
 Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg  
 115 120 125  
 Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln  
 130 135 140  
 Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys  
 145 150 155 160  
 Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala  
 165 170 175  
 Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys  
 180 185 190  
 Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro  
 195 200 205  
 Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp  
 210 215 220  
 Glu Glu Lys Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile  
 225 230 235 240  
 Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu  
 245 250

<210> 84  
 <211> 3494  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <221> CDS  
 <222> (2411) .. (2719)

<220>  
 <223> yyaM

<400> 84  
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 gaaaatgctt tacgcgaata tggttgttat ctaggcacag cttttcaatt agtcgatgat 180

attttagatt atagtgcaga tgcaaaagca ctcggaacaa atattggtga tgatttagcg 240  
 gaaggtaaac caacattacc gttattacac gccatgcac acggcaatcc agcacaagca 300  
 aaattgattc gcgaagcgat tgagcaaggg ggtaagcgtg atattttaga ggatgtactg 360  
 acaattatga cagaacataa atccctcgac tatgcgcatga tgcgcgctaa acaagaagca 420  
 caaaaagccg ttgatgcgat tgcattattg cctgaaaaat aatataaaca agcgttaatt 480  
 tcattagctt acttatccgt cgatcgcgct tattaaccac ttaataaggc gagacatggt 540  
 agcgtaacga ccgcctaag tgccggtcatt tattttagtaa ttttaaacac gacaatgaca 600  
 gaacaaaaca tccctacgaa aaaaacacgc aaaggcaag atccctacgc gccctttgta 660  
 cgcgaaaaat tatccctacc aaatgggcat acaaatgtg tattgcattc ttgtgtgctg 720  
 ccttgctcgg gagaagtaat ggaggcaatt catgcttcag gtattgaatt tactatttac 780  
 ttctacaacc caaacattca cccattaaaa gaatatctca ttcgtaaga agaaaatatt 840  
 cgttttgcgg aaaaatgggg cattccgttt attgatgcg attatgatcg tcaagaatgg 900  
 tttagccgtg ccaaaaggcat ggaagatgag ccagagcgtg gtattcgttg cactatgtgc 960  
 ttgatatgc gttttgaaa agccgcagaa tatgcacaca acaatggttt ccccgatatt 1020  
 actagctgct taggtatttc acgttggaaa gacatgaacc aaatcaacgg ttgtggacac 1080  
 cgtgccgcgc aaaaatatga tgatgtatg tattgggatt ataactggcg taaaggtggt 1140  
 ggctcacaac gtatgattga aatcagtaag cgtgaacgtt ttaccagca agaattattg 1200  
 ggttggtgtg attcttttgc tgacacgaat aaatggcgtg aagcaaacgg acgcaaaaa 1260  
 attgaaattg gcaaattgta ttattccgcc gattaaaaa accaagtaaa ccattcgtgc 1320  
 gtcataatac atggcggcac ttttttagc tttatatatg caacgttttc gccaatcttt 1380  
 cgaaacctaa tgctaacgcc tcttactaa tatttaatgc tggggcaaaa cgcaatacat 1440  
 taggaccgc cactaaaatc attagccat tatctgctgc tttttgaca aattcgctcg 1500  
 ctctccgtg atattgctg ataagttctg caccaattaa caaaccttcg ccacggattt 1560  
 ctttaataa gccacattgc tgattaattt ctgcagctt ttgcataat ttttcagaag 1620  
 tgcgctgaat tttttgcaag aatggtggtg ctgaaatgat atcaatcact ttttctgcca 1680  
 cggcacaagc gagaggattg ccaccaaaag tgggtgccatg caccgcaagt gcaaaacttt 1740  
 tggcgatctc atgcgttgtc aacgaatgag aaaaattgta cagattgggc tccaacggga 1800  
 cgtgcggatg agattgggga tacgcaagta cgttatgaa ttgagcaggt gagttctagc 1860  
 aattatagtg cactgtttgt ctccatttta cagatgaac gtaatgaggt ggtatttagt 1920  
 ccacatttag cggataaaca acgttatagt tctgatcgct tgaaccaact tgttggtgaa 1980  
 tttagatcgt cttatcgtaa acaagtcctg gatttgaata acagcggatt gatccaatt 2040

cagctctgatat tcggtacgga cagtaaatggg cgtactgctc tcgtgttagg cgcacccttt 2100  
 aatcatgcgt ggacaaaact aggacaagtt ttaccgcagc ttgaatttga tattaagat 2160  
 gaaattattg gtcgtggggg aagggaagta aaataccgctc cagctggagc aaaaagttgg 2220  
 tgggtggccat ttggtcgtgc tgaaggcagt agcggactga aaacaggtag ctattttatg 2280  
 cagttaagcg ccttagggaa gcaaagtgcg gtggtgatga ccgatgatga tggcaatgcg 2340  
 ttatctgggg agcaagctca gccgctttat caagcattac aaaaatctct agcgaaataa 2400  
 tacagtcaag atg act aaa ctc agt atc cag cga gat aac ttg att tgt 2449  
     Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys  
     1                    5                    10  
 ttg agt tat gtc gca tta atg gga ttc gcc ttt ccc att atg cgt tat 2497  
 Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr  
     15                    20                    25  
 atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc 2545  
 Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu  
     30                    35                    40                    45  
 tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593  
 Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala  
     50                    55                    60  
 gag tta aca tct tcg ggg gct gcc gtc cag tcc gtt gcg atg ttg ccg 2641  
 Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro  
     65                    70                    75  
 agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca 2689  
 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser  
     80                    85                    90  
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcg atttttgata 2739  
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val  
     95                    100  
 gtcaaagact actgagtaac gcttgtagtc gcgtgaatcg actgttacat aagccgatat 2799  
 gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttggt 2859  
 cgataaagcg tcaaacgaaa gcacgacttt accgctccttg acttccacct gatcttcaat 2919  
 gagcaactga cttagtgcga ccaatcgacc gttaggcagtc agtgctgcga tgccgtgatc 2979  
 cgtatcaagc gttacaccgc tattttttcc ccagttttta ttgagctttt cactatggtt 3039  
 cagtaagttt ctgccaccaa tctgcaactg attaaactta gcttcaagcg tttcactctt 3099  
 gactgcaagc gaactgtttt cattgctaac cgtctgctca agtgctgtga ttttgatgt 3159  
 taaatctaac ttagtgtcat tgacttcac cagtcattct gactttaact cttttctcgc 3219  
 aagtgcgccc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279  
 attttgcgcc actttagaat cgagcgtttc tagttttgta gagaagatt tgtctttttc 3339  
 gctagcgtt ttttgaatta gctgtatttc actttcgcgc aatccaactc tagcagttag 3399

actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459

aatatccgcg cttacttcgc agatagccac gtcga 3494

<210> 85

<211> 103

<212> PRT

<213> Pasteurella multocida

<400> 85

Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys Leu Ser Tyr  
1 5 10 15

Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr Met Ser Ile  
20 25 30

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly  
35 40 45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr  
50 55 60

Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro Ser Ser Ser  
65 70 75 80

Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser Tyr Val Thr  
85 90 95

Ile Ser Thr Leu Asn Arg Val  
100

<210> 86

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 86

aggccggtac cggccgctt 19

<210> 87

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 87

cggccggtac cggcctagg 19

<210> 88

<211> 18

<212> DNA

<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 88  
catggtaccc attctaac 18

<210> 89  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 89  
ctaggtacct acaacctc 18

<210> 90  
<211> 119  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: transposon  
insert

<400> 90  
ctaggtacct acaacctcaa gcttnknknk nknknknknk nknknknknk nknknknknk 60  
nknknknknk nknknknknk nknknknknk nknkaagctt gggttagaatg ggtaccatg 119

<210> 91  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 91  
tacctacaac ctcaagct 18

<210> 92  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: primer

<400> 92  
taccattct aaccaagc 18

<210> 93  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 93  
 tacctacaac ctcaagctt 19  
  
 <210> 94  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 94  
 taccattct aaccaagctt 20  
  
 <210> 95  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 95  
 ggcagagcat tacgctgac 19  
  
 <210> 96  
 <211> 27  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Description of Artificial Sequence: primer  
  
 <400> 96  
 gtaccggcca ggcggccacg cgtattc 27  
  
 <210> 97  
 <211> 531  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae  
  
 <220>  
 <223> atpG  
  
 <400> 97  
 tgttgagctt ggttagtag ggtcgaaagg cgtaagcttt taccaaaatc taggcttaa 60  
 cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggccc 120  
 agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcgggtt acgtcgctta 180  
 caaccgtttt gaaaatacga tgtcacaaaa acctgttatc gcacagttac ttccgttacc 240  
 taaactagat gacgatgaat tagatacgaa aggttcatgg gattatatatt atgaaccgaa 300

tccacaagtt ttattggata gtttacttgt tcgttattha gaaactcagg tataccaagc 360  
 agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420  
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcgccaagc 480  
 aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98  
 <211> 25  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 98  
 tctccattcc ctgctgcgg caccc 25

<210> 99  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: primer

<400> 99  
 ggattacagc cggatccggg 20

<210> 100  
 <211> 1034  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> cap5E

<220>  
 <221> CDS  
 <222> (1)..(1032)

<400> 100  
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 Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe  
 1 5 10 15  
 ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96  
 Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile  
 20 25 30  
 cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144  
 Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys  
 35 40 45  
 tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192  
 Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr  
 50 55 60

gat agt att tta aat gcc tgc cga ggt gtt gac tat att tat cat gct	240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala	
65 70 75 80	
gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca	288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala	
85 90 95	
gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc	336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile	
100 105 110	
caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg	384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val	
115 120 125	
tac cca att aat gcg atg gcc att tct aaa gca atg atg gaa aaa gtc	432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val	
130 135 140	
atc atc gca aaa tgc cgt aac cta gaa ggc aca cca acg aca atc tgt	480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys	
145 150 155 160	
tgt act cgc tat gcc aat gtc atg gca tgc cgt ggt tgc gtt atc cca	528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro	
165 170 175	
tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat	576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp	
180 185 190	
cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta	624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu	
195 200 205	
gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa	672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln	
210 215 220	
aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa	720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu	
225 230 235 240	
tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat	768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His	
245 250 255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat	816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His	
260 265 270	
gca att aat gaa ggt aat tat tat cgc atc cca gcc gat caa cgc agt	864
Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser	
275 280 285	
tta aat tac agt aaa tat gtc gaa aaa ggg gaa cca aaa att acc gaa	912
Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu	
290 295 300	
gtc acc gac tac aac tca cat aat act gag cgt ttg act gtc aag gaa	960
Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu	



Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His  
 245 250 255  
 Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His  
 260 265 270  
 Ala Ile Asn Glu Gly Asn Tyr Tyr Arg Ile Pro Ala Asp Gln Arg Ser  
 275 280 285  
 Leu Asn Tyr Ser Lys Tyr Val Glu Lys Gly Glu Pro Lys Ile Thr Glu  
 290 295 300  
 Val Thr Asp Tyr Asn Ser His Asn Thr Glu Arg Leu Thr Val Lys Glu  
 305 310 315 320  
 Met Lys Gln Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu  
 325 330 335  
 Gly Glu Tyr Ile Ser Pro Glu Val  
 340

<210> 102  
 <211> 4931  
 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <223> fhaB2

<220>  
 <221> CDS  
 <222> (1) .. (4929)

<400> 102  
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 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys  
 1 5 10 15  
 ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96  
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser  
 20 25 30  
 tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt 144  
 Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Val Pro Phe Leu  
 35 40 45  
 cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg 192  
 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr  
 50 55 60  
 ttc aat cct gtt tgg tat gca atg caa ttg act tgg aaa cag ctt tct 240  
 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser  
 65 70 75 80  
 att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa 288  
 Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys  
 85 90 95  
 ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att 336  
 Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
 100 105 110

aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr	384
115 120 125	
caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly	432
130 135 140	
aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser	480
145 150 155 160	
gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu	528
165 170 175	
att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala	576
180 185 190	
gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val	624
195 200 205	
ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn	672
210 215 220	
caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg	720
225 230 235 240	
ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu	768
245 250 255	
aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr	816
260 265 270	
gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	864
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	912
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	960
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	1008
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	1056
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	1104

355	360	365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg 1152 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr 370 375 380			
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aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg 1248 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr 405 410 415			
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa 1296 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys 420 425 430			
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt 1344 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly 435 440 445			
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat 1392 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp 450 455 460			
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag 1440 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu 465 470 475 480			
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct 1488 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala 485 490 495			
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att 1536 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile 500 505 510			
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc 1584 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg 515 520 525			
ttt tta ggc tct cgg ttt ttc tca ata tct cgg tcg atg ctc gca agc 1632 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser 530 535 540			
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa 1680 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu 545 550 555 560			
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta 1728 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu 565 570 575			
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac 1776 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn 580 585 590			
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct 1824 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala 595 600 605			

aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr 610 615 620	1872
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile 625 630 635 640	1920
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr 645 650 655	1968
gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Ala Glu Asn 660 665 670	2016
ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser 675 680 685	2064
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His 690 695 700	2112
act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr 705 710 715 720	2160
aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val 725 730 735	2208
cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu 740 745 750	2256
caa gat aaa acc gat att aaa gtt gtg aaa atg ggc gct atc cgt tct Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser 755 760 765	2304
gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser 770 775 780	2352
aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe 785 790 795 800	2400
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aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr 820 825 830	2496
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850	855	860	
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt 2640			
Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser			
865	870	875	880
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa 2688			
Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys			
	885	890	895
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat 2736			
Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp			
	900	905	910
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Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe			
	915	920	925
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa 2832			
Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu			
	930	935	940
ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag 2880			
Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys			
	945	950	955
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Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp			
	980	985	990
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Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu			
	995	1000	1005
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Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Leu Ser Pro Ile			
	1010	1015	1020
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Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser			
	1025	1030	1035
cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct 3168			
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser			
	1045	1050	1055
gat aca gac gat agc aag tgg agt atg gcc aat gat gag aaa gag atg 3216			
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met			
	1060	1065	1070
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca 3264			
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro			
	1075	1080	1085
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt 3312			
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe			
	1090	1095	1100

gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu 1105 1110 1115 1120	3360
cgg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu 1125 1130 1135	3408
gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys 1140 1145 1150	3456
gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu 1155 1160 1165	3504
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg 1170 1175 1180	3552
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aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg 1220 1225 1230	3696
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caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser 1285 1290 1295	3888
aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu 1300 1305 1310	3936
act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp 1315 1320 1325	3984
tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys 1330 1335 1340	4032
ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln 1345 1350 1355	4080

1345	1350	1355	1360	
gtg att act cgc tgc att gag aaa aaa gta gat aac cac ctt aac caa				4128
Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln	1365	1370	1375	
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat				4176
Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn	1380	1385	1390	
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta				4224
Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu	1395	1400	1405	
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Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val	1410	1415	1420	
aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc				4320
Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe	1425	1430	1435	1440
gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act				4368
Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr	1445	1450	1455	
ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg				4416
Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	1460	1465	1470	
aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat				4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	1475	1480	1485	
aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta				4512
Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu	1490	1495	1500	
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat				4560
Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	1505	1510	1515	1520
gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat				4608
Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His	1525	1530	1535	
tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tgc				4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	1540	1545	1550	
gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc				4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu	1555	1560	1565	
aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tgc ccg				4752
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro	1570	1575	1580	
agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca				4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro	1585	1590	1595	1600

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 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val  
 1605 1610 1615

agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt 4896  
 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa  
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<211> 1643

<212> PRT

<213> Pasteurella multocida

<400> 103

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Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu  
 35 40 45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr  
 50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser  
 65 70 75 80

Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys  
 85 90 95

Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile  
 100 105 110

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr  
 115 120 125

Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly  
 130 135 140

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser  
 145 150 155 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu  
 165 170 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala  
 180 185 190

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val  
 195 200 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn  
 210 215 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg

225	230	235	240
Phe Val Ala Thr Thr 245	Ser Glu Leu Ile Asp 250	Pro Asn Gln Met 255	Met Leu
Lys Val Thr Lys Gly 260	Asn Val Ile Ile Asp 265	Ile Asp Gly Phe Ser Thr 270	
Asp Gly Leu Lys Tyr 275	Leu Asp Ile Ile Ala 280	Lys Lys Ile Glu Gln Lys 285	
Gln Ser Ile Thr Ser 290	Gly Asp Asn Ser Glu 295	Ala Lys Thr Asp Val Thr 300	
Leu Ile Ala Gly Ser 305	Ser Glu Tyr Asp Leu 310	Ser Lys His Glu Leu Lys 315	
Lys Thr Ser Gly Glu 325	Asn Val Ser Asn Asp 330	Val Ile Ala Ile Thr Gly 335	
Ser Ser Thr Gly Ala 340	Met His Gly Lys Asn 345	Ile Lys Leu Ile Val Thr 350	
Asp Lys Gly Ala Gly 355	Val Lys His Asp Gly 360	Ile Ile Leu Ser Glu Asn 365	
Asp Ile Gln Ile Glu 370	Met Asn Glu Gly Asp 375	Leu Glu Leu Gly Asn Thr 380	
Ile Gln Gln Thr Val 385	Val Lys Lys Asp Arg 390	Asn Ile Arg Ala Lys Lys 395	
Lys Ile Glu Val Lys 405	Asn Ala Asn Arg Val 410	Phe Val Gly Ser Gln Thr 415	
Lys Ser Asp Glu Ile 420	Ser Leu Glu Ala Lys 425	Gln Val Lys Ile Arg Lys 430	
Asn Ala Glu Ile Arg 435	Ser Thr Thr Gln Ala 440	Lys Ile Val Ala Lys Gly 445	
Ala Leu Ser Ile Glu 450	Gln Asn Ala Lys Leu 455	Val Ala Lys Lys Ile Asp 460	
Val Ala Thr Glu Thr 465	Leu Thr Asn Ala Gly 470	Arg Ile Tyr Gly Arg Glu 475	
Val Lys Leu Asp Thr 485	Asn Asn Leu Ile Asn 490	Asp Lys Glu Ile Tyr Ala 495	
Glu Arg Lys Leu Ser 500	Ile Leu Thr Lys Gly 505	Lys Asp Leu Glu Ile Ile 510	
Gln Asp Arg Tyr Leu 515	Ser Pro Leu Met Arg 520	Val Lys Ser Ser Val Arg 525	
Phe Leu Gly Ser Pro 530	Phe Ser Ile Ser Pro 535	Ser Met Leu Ala Ser 540	
Leu Ser Ala Gln Phe 545	Lys Pro Gly Phe Val 550	Asn Lys Gly Leu Ile Glu 555	
			560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu  
 565 570 575  
 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn  
 580 585 590  
 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala  
 595 600 605  
 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr  
 610 615 620  
 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile  
 625 630 635 640  
 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr  
 645 650 655  
 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn  
 660 665 670  
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser  
 675 680 685  
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His  
 690 695 700  
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr  
 705 710 715 720  
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val  
 725 730 735  
 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu  
 740 745 750  
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser  
 755 760 765  
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser  
 770 775 780  
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe  
 785 790 795 800  
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 805 810 815  
 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr  
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 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala  
 835 840 845  
 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly  
 850 855 860  
 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser  
 865 870 875 880  
 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys  
 885 890 895

Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp  
900 905 910

Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe  
915 920 925

Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu  
930 935 940

Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys  
945 950 955 960

Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser  
965 970 975

Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp  
980 985 990

Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu  
995 1000 1005

Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile  
1010 1015 1020

Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser  
1025 1030 1035 1040

His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser  
1045 1050 1055

Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met  
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Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro  
1075 1080 1085

Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe  
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Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu  
1105 1110 1115 1120

Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu  
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Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys  
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Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu  
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Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala  
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Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg  
1220 1225 1230

Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys  
 1235 1240 1245  
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 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu  
 1265 1270 1275 1280  
 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser  
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 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu  
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 Thr Asp Thr Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp  
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 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys  
 1330 1335 1340  
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln  
 1345 1350 1355 1360  
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln  
 1365 1370 1375  
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn  
 1380 1385 1390  
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu  
 1395 1400 1405  
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val  
 1410 1415 1420  
 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe  
 1425 1430 1435 1440  
 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr  
 1445 1450 1455  
 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val  
 1460 1465 1470  
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn  
 1475 1480 1485  
 Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu  
 1490 1495 1500  
 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp  
 1505 1510 1515 1520  
 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His  
 1525 1530 1535  
 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser  
 1540 1545 1550  
 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu  
 1555 1560 1565

Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro  
 1570 1575 1580

Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro  
 1585 1590 1595 1600

Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val  
 1605 1610 1615

Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa  
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<220>  
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<220>  
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 <222> (1)..(2007)

<400> 104  
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cgc cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96  
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu  
 20 25 30

cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144  
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser  
 35 40 45

ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192  
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala  
 50 55 60

tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240  
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val  
 65 70 75 80

gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca 288  
 Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser  
 85 90 95

aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa 336  
 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Lys Gly Glu  
 100 105 110

cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca 384  
 His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr  
 115 120 125

atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa 432

Ile	Asn	Asn	Gly	Lys	Gly	Thr	Asp	Ile	Leu	Gly	Glu	His	Arg	Gly	Lys		
130						135					140						
ccc	aat	ccg	ctc	aac	tac	tat	act	aca	tca	tgg	tta	acg	aaa	gtc	ggg	480	
Pro	Asn	Pro	Leu	Asn	Tyr	Tyr	Thr	Thr	Ser	Trp	Leu	Thr	Lys	Val	Gly		
145					150					155				160			
tac	gat	att	aat	aac	act	cat	cgt	ttt	aca	ctg	ttt	tta	gaa	gat	cgc	528	
Tyr	Asp	Ile	Asn	Asn	Thr	His	Arg	Phe	Thr	Leu	Phe	Leu	Glu	Asp	Arg		
				165				170						175			
cgt	gaa	aag	aag	ctt	acc	gaa	gaa	aaa	aca	tta	ggg	ctt	agt	gat	gca	576	
Arg	Glu	Lys	Lys	Leu	Thr	Glu	Glu	Lys	Thr	Leu	Gly	Leu	Ser	Asp	Ala		
				180				185						190			
gtg	cgt	ttt	gct	aat	gat	caa	acc	cct	tat	ctc	cgt	tat	ggg	att	gaa	624	
Val	Arg	Phe	Ala	Asn	Asp	Gln	Thr	Pro	Tyr	Leu	Arg	Tyr	Gly	Ile	Glu		
		195				200						205					
tat	cga	tat	aac	ggc	ttg	tct	tgg	ttg	gaa	acg	gta	aag	ctt	ttt	ttg	672	
Tyr	Arg	Tyr	Asn	Gly	Leu	Ser	Trp	Leu	Glu	Thr	Val	Lys	Leu	Phe	Leu		
	210					215					220						
gca	aag	cag	aaa	atc	gaa	caa	cgt	tct	gct	ctc	caa	gag	ttt	gat	att	720	
Ala	Lys	Gln	Lys	Ile	Glu	Gln	Arg	Ser	Ala	Leu	Gln	Glu	Phe	Asp	Ile		
225				230					235					240			
aat	aat	agg	aat	aaa	ttg	gat	tcg	act	atg	tcg	ttt	gta	tat	tta	caa	768	
Asn	Asn	Arg	Asn	Lys	Leu	Asp	Ser	Thr	Met	Ser	Phe	Val	Tyr	Leu	Gln		
				245				250						255			
aga	cag	aat	ata	gct	cgg	gga	gaa	ttt	tca	acg	agt	cct	tta	tat	ttg	816	
Arg	Gln	Asn	Ile	Ala	Arg	Gly	Glu	Phe	Ser	Thr	Ser	Pro	Leu	Tyr	Trp		
			260					265					270				
ggg	ccg	agt	cgc	cat	cgt	tta	tct	gcg	aaa	ttc	gaa	ttt	cgt	gat	aag	864	
Gly	Pro	Ser	Arg	His	Arg	Leu	Ser	Ala	Lys	Phe	Glu	Phe	Arg	Asp	Lys		
		275				280						285					
ttt	tta	gaa	aat	atg	aat	aag	cat	ttt	acg	ttt	cgg	ccg	ttg	caa	atc	912	
Phe	Leu	Glu	Asn	Met	Asn	Lys	His	Phe	Thr	Phe	Arg	Pro	Trp	Gln	Ile		
	290					295					300						
aat	aga	ttc	aga	caa	caa	ggg	cga	aat	aac	tat	aca	gaa	gtg	ttt	ccc	960	
Asn	Arg	Phe	Arg	Gln	Gln	Gly	Arg	Asn	Asn	Tyr	Thr	Glu	Val	Phe	320		
305					310				315								
gtt	aaa	tcc	cga	gag	ttt	tct	ttt	tct	ctt	atg	gac	gac	att	aag	att	1008	
Val	Lys	Ser	Arg	Glu	Phe	Ser	Phe	Ser	Leu	Met	Asp	Asp	Ile	Lys	Ile		
				325				330					335				
ggc	gaa	ttg	cta	cat	ctc	gga	ttg	ggc	ggg	cgg	ttg	gat	cac	tat	aac	1056	
Gly	Glu	Leu	Leu	His	Leu	Gly	Leu	Gly	Arg	Trp	Asp	His	Tyr	Asn			
			340					345					350				
tat	aag	cca	tta	tta	aat	tct	cag	cat	aat	atc	aac	agg	aca	cag	aga	1104	
Tyr	Lys	Pro	Leu	Leu	Asn	Ser	Gln	His	Asn	Ile	Asn	Arg	Thr	Gln	Arg		
		355				360						365					
tta	cct	tat	cca	aaa	aca	tca	tcc	aaa	ttt	tcg	tat	caa	ttg	agt	tta	1152	
Leu	Pro	Tyr	Pro	Lys	Thr	Ser	Ser	Lys	Phe	Ser	Tyr	Gln	Leu	Ser	Leu		
	370					375					380						

gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr 385 390 395 400	1200
ggg ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly 405 410 415	1248
aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr 420 425 430	1296
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His 435 440 445	1344
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu 450 455 460	1392
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr 465 470 475 480	1440
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu 485 490 495	1488
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tgg gca Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala 500 505 510	1536
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser 515 520 525	1584
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp 530 535 540	1632
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser 545 550 555 560	1680
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu 565 570 575	1728
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu 580 585 590	1776
agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser 595 600 605	1824
aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp 610 615 620	1872
tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr	1920

625 630 635 640

tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968  
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala  
 645 650 655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009  
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe  
 660 665

<210> 105  
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 <212> FRT  
 <213> *Pasteurella multocida*

<400> 105  
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 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu  
 20 25 30  
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser  
 35 40 45  
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala  
 50 55 60  
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val  
 65 70 75 80  
 Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser  
 85 90 95  
 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu  
 100 105 110  
 His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr  
 115 120 125  
 Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys  
 130 135 140  
 Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly  
 145 150 155 160  
 Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg  
 165 170 175  
 Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala  
 180 185 190  
 Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu  
 195 200 205  
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu  
 210 215 220  
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile  
 225 230 235 240

Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln  
 245 250 255  
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp  
 260 265 270  
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys  
 275 280 285  
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile  
 290 295 300  
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro  
 305 310 315 320  
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile  
 325 330 335  
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn  
 340 345 350  
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg  
 355 360 365  
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu  
 370 375 380  
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr  
 385 390 395 400  
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly  
 405 410 415  
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr  
 420 425 430  
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His  
 435 440 445  
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu  
 450 455 460  
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr  
 465 470 475 480  
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu  
 485 490 495  
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala  
 500 505 510  
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser  
 515 520 525  
 Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp  
 530 535 540  
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser  
 545 550 555 560  
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu  
 565 570 575

Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu  
580 585 590

Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser  
595 600 605

Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp  
610 615 620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr  
625 630 635 640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala  
645 650 655

Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe  
660 665

<210> 106  
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<212> DNA  
<213> Pasteurella multocida

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<220>  
<221> CDS  
<222> (1)..(906)

<400> 106  
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gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96  
Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144  
Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192  
Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
50 55 60

gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240  
Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288  
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
85 90 95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336  
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
100 105 110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384  
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys

115	120	125	
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att			432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile			
130	135	140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt			480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe			
145	150	155	160
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac			528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp			
165	170		175
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata			576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile			
180	185		190
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt			624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe			
195	200		205
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga			672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly			
210	215		220
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt			720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val			
225	230		235
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa			768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys			
245	250		255
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga			816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg			
260	265		270
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc			864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala			
275	280		285
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta			908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr			
290	295		300

<210> 107  
 <211> 302  
 <212> PRT  
 <213> Pasteurella multocida

<400> 107  
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 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe  
 20 25 30  
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn  
 35 40 45

Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn  
 50 55 60  
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu  
 65 70 75 80  
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu  
 85 90 95  
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu  
 100 105 110  
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys  
 115 120 125  
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile  
 130 135 140  
 Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe  
 145 150 155 160  
 Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp  
 165 170 175  
 Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile  
 180 185 190  
 Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe  
 195 200 205  
 Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly  
 210 215 220  
 Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val  
 225 230 235 240  
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys  
 245 250 255  
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg  
 260 265 270  
 Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala  
 275 280 285  
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 290 295 300

<210> 108  
 <211> 2054  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> pnp

<220>  
 <221> CDS  
 <222> (1) ..(2052)

<400> 108

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Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys	
1 5 10 15	
aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat	96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr	
20 25 30	
caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa	144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Phe Phe Lys	
35 40 45	
cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att	192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile	
50 55 60	
gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc	240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Thr Phe Tyr Asn Glu Ile	
65 70 75 80	
caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat	288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp	
85 90 95	
tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg	336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val	
100 105 110	
cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat	384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp	
115 120 125	
caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta	432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu	
130 135 140	
gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct	480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser	
145 150 155 160	
gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt	528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe	
165 170 175	
ggg cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc	576
Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr	
180 185 190	
gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat	624
Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn	
195 200 205	
acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc	672
Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly	
210 215 220	
gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat	720
Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp	
225 230 235 240	
gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa	768
Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu	

245	250	255	
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt 816 Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu 260 265 270			
gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att 864 Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile 275 280 285			
gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt 912 Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly 290 295 300			
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca 960 Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr 305 310 315 320			
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att 1008 Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile 325 330 335			
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac 1056 Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr 340 345 350			
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca 1104 Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro 355 360 365			
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct 1152 Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380			
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc 1200 Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400			
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tcg gtt tgt 1248 Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys 405 410 415			
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg 1296 Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430			
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg 1344 Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445			
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac 1392 Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460			
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat 1440 Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480			
atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac 1488 Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495			

caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg 1536  
 Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala  
 500 505 510  
 atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac 1584  
 Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr  
 515 520 525  
 act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt 1632  
 Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly  
 530 535 540  
 ggt gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat 1680  
 Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp  
 545 550 555 560  
 atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca 1728  
 Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser  
 565 570 575  
 gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa 1776  
 Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu  
 580 585 590  
 gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt 1824  
 Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly  
 595 600 605  
 gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct 1872  
 Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser  
 610 615 620  
 caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg 1920  
 Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val  
 625 630 635 640  
 ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt 1968  
 Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg  
 645 650 655  
 att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat 2016  
 Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp  
 660 665 670  
 tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta 2054  
 Ser Val Val Ala Asp Val Ala Glu Glu Asn Ala  
 675 680

<210> 109  
 <211> 684  
 <212> PRT  
 <213> Pasteurella multocida

<400> 109  
 Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys  
 1 5 10 15  
 Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr  
 20 25 30  
 Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys

35 40 45

Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile  
50 55 60

Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile  
65 70 75 80

Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp  
85 90 95

Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val  
100 105 110

Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp  
115 120 125

Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu  
130 135 140

Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser  
145 150 155 160

Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe  
165 170 175

Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr  
180 185 190

Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn  
195 200 205

Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly  
210 215 220

Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp  
225 230 235 240

Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu  
245 250 255

Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu  
260 265 270

Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile  
275 280 285

Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly  
290 295 300

Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr  
305 310 315 320

Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile  
325 330 335

Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr  
340 345 350

Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro  
355 360 365

Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala  
 370 375 380  
 Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val  
 385 390 395 400  
 Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Met Ala Ser Val Cys  
 405 410 415  
 Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala  
 420 425 430  
 Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val  
 435 440 445  
 Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp  
 450 455 460  
 Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp  
 465 470 475 480  
 Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn  
 485 490 495  
 Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala  
 500 505 510  
 Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr  
 515 520 525  
 Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly  
 530 535 540  
 Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp  
 545 550 555 560  
 Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser  
 565 570 575  
 Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu  
 580 585 590  
 Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly  
 595 600 605  
 Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser  
 610 615 620  
 Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val  
 625 630 635 640  
 Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg  
 645 650 655  
 Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp  
 660 665 670  
 Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala  
 675 680

<210> 110

<211> 1514  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> purF

<220>  
 <221> CDS  
 <222> (1) .. (1512)

<400> 110  
 atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48  
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser 15  
 1 5 10  
 att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96  
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala 20 25 30  
 ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144  
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala 35 40 45  
 aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192  
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu 50 55 60  
 caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240  
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser 65 70 75 80  
 tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288  
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly 85 90 95  
 tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336  
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys 100 105 110  
 gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384  
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp 115 120 125  
 tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432  
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu 130 135 140  
 aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480  
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr 145 150 155 160  
 cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528  
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly 165 170 175  
 cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576  
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val 180 185 190  
 tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624  
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

195

200

205

gaa agt atc gca tta gat Glu Ser Ile Ala Leu Asp 210	aca gtg ggt ttt gag ttt gta cga gat gta Thr Val Gly Phe Glu Val Arg Asp Val 215	672
caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala 225 230 235 240		720
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr 245 250 255		768
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr 260 265 270		816
gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg 275 280 285		864
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu 290 295 300		912
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro 305 310 315 320		960
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile 325 330 335		1008
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn 340 345 350		1056
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp 355 360 365		1104
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg 370 375 380		1152
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile 385 390 395 400		1200
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu 405 410 415		1248
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val 420 425 430		1296
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln 435 440 445		1344

caa gaa aat cca agt att caa gac ttt gat tgt tct gtg ttt aca ggg 1392  
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460

gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca 1440  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480

gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc 1488  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495

aat ctt gaa atg cac aat gaa aaa ta 1514  
 Asn Leu Glu Met His Asn Glu Lys  
 500

<210> 111  
 <211> 504  
 <212> PRT  
 <213> *Pasteurella multocida*

<400> 111  
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser  
 1 5 10 15

Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala  
 20 25 30

Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala  
 35 40 45

Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu  
 50 55 60

Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser  
 65 70 75 80

Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly  
 85 90 95

Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys  
 100 105 110

Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp  
 115 120 125

Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu  
 130 135 140

Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr  
 145 150 155 160

His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly  
 165 170 175

His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val  
 180 185 190

Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser  
 195 200 205

Glu Ser Ile Ala Leu Asp Thr Val Gly Phe Glu Phe Val Arg Asp Val  
 210 215 220  
 Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala  
 225 230 235 240  
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr  
 245 250 255  
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr  
 260 265 270  
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg  
 275 280 285  
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu  
 290 295 300  
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro  
 305 310 315 320  
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile  
 325 330 335  
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn  
 340 345 350  
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp  
 355 360 365  
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg  
 370 375 380  
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile  
 385 390 395 400  
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu  
 405 410 415  
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val  
 420 425 430  
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln  
 435 440 445  
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly  
 450 455 460  
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala  
 465 470 475 480  
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr  
 485 490 495  
 Asn Leu Glu Met His Asn Glu Lys  
 500

<210> 112  
 <211> 989  
 <212> DNA  
 <213> Pasteurella multocida

<220>

<223> rci

<220>

<221> CDS

<222> (1) .. (987)

<400> 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc 48  
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser  
1 5 10 15

aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct 96  
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala  
20 25 30

aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa 144  
Asn Ala Trp Ala Val Asp Glu Arg Lys Leu Ala Asp Leu Ala Lys  
35 40 45

ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa 192  
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln  
50 55 60

aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga 240  
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg  
65 70 75 80

tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat 288  
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp  
85 90 95

tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa 336  
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu  
100 105 110

gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg 384  
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val  
115 120 125

ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg 432  
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met  
130 135 140

act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat 480  
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr  
145 150 155 160

tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa 528  
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu  
165 170 175

gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta 576  
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu  
180 185 190

ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa 624  
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys  
195 200 205

tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act 672  
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr

210	215	220	
aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg			720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala			
225	230	235	240
cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag			768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln			
	245	250	255
acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag			816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu			
	260	265	270
tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg			864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu			
	275	280	285
acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc			912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser			
	290	295	300
gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat			960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn			
	305	310	315
atg agt gaa gtg gca aac ttg ttg gat ta			989
Met Ser Glu Val Ala Asn Leu Leu Asp			
	325		
<210> 113			
<211> 329			
<212> PRT			
<213> Pasteurella multocida			
<400> 113			
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser			
1	5	10	15
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala			
	20	25	30
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys			
	35	40	45
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln			
	50	55	60
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg			
	65	70	75
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp			
	85	90	95
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu			
	100	105	110
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val			
	115	120	125
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met			

130 135 140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr  
145 150 155 160

Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu  
165 170 175

Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu  
180 185 190

Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys  
195 200 205

Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr  
210 215 220

Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala  
225 230 235 240

Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln  
245 250 255

Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu  
260 265 270

Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu  
275 280 285

Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser  
290 295 300

Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn  
305 310 315 320

Met Ser Glu Val Ala Asn Leu Leu Asp  
325

<210> 114  
<211> 1190  
<212> DNA  
<213> Pasteurella multocida

<220>  
<223> sopE

<220>  
<221> CDS  
<222> (1)..(1188)

<400> 114  
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa 48  
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln  
1 5 10 15

gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc 96  
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
20 25 30

tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc 144  
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro

35	40	45	
gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa 192 Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln 50 55 60			
ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc aat tgc 240 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys 65 70 75 80			
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa 288 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu 85 90 95			
aca aaa gca agt gaa atg aac acg gca att att ggc aca atc aca gaa 336 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu 100 105 110			
gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa aac aaa 384 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys 115 120 125			
ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa 432 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys 130 135 140			
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt 480 Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe 145 150 155 160			
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa 528 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln 165 170 175			
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg ggc gat 576 Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp 180 185 190			
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc 624 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala 195 200 205			
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag ggc 672 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly 210 215 220			
tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc ggt gtc 720 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val 225 230 235 240			
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac 768 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn 245 250 255			
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat ggc ttt 816 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe 260 265 270			
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt 864 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe 275 280 285			

gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg 912  
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly  
 290 295 300

gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta gtg aaa 960  
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys  
 305 310 315 320

gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa 1008  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335

ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056  
 Gly Tyr Leu Ile Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350

gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365

cca gta cca cgc ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395

<210> 115  
 <211> 396  
 <212> PRT  
 <213> Pasteurella multocida

<400> 115  
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 Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val  
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 Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro  
 35 40 45  
 Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln  
 50 55 60  
 Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys  
 65 70 75 80  
 Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu  
 85 90 95  
 Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu  
 100 105 110  
 Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys  
 115 120 125  
 Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys  
 130 135 140

Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe  
 145 150 155 160  
 Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln  
 165 170 175  
 Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp  
 180 185 190  
 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala  
 195 200 205  
 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly  
 210 215 220  
 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val  
 225 230 235 240  
 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn  
 245 250 255  
 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe  
 260 265 270  
 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe  
 275 280 285  
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly  
 290 295 300  
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys  
 305 310 315 320  
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys  
 325 330 335  
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser  
 340 345 350  
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His  
 355 360 365  
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp  
 370 375 380  
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser  
 385 390 395

<210> 116  
 <211> 2204  
 <212> DNA  
 <213> *Pasteurella multocida*

<220>  
 <223> unkK

<220>  
 <221> CDS  
 <222> (1) .. (2202)

<400> 116

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Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys	
1 5 10 15	
ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca	96
Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser	
20 25 30	
tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc	144
Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu	
35 40 45	
aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat	192
Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn	
50 55 60	
ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta	240
Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu	
65 70 75 80	
tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca	288
Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr	
85 90 95	
gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc	336
Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser	
100 105 110	
aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat	384
Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His	
115 120 125	
caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att	432
Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile	
130 135 140	
gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc	480
Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe	
145 150 155 160	
aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc	528
Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg	
165 170 175	
tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt	576
Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly	
180 185 190	
agt gaa gca aaa gcg atc tta aat cag gtg act gga cgg gat gcc agt	624
Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser	
195 200 205	
aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg	672
Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val	
210 215 220	
att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat	720
Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn	
225 230 235 240	
gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa	768
Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln	

245										250										255									
atg	cag	tta	aat	gtc	acg	caa	ggg	aca	gtg	aca	att	ggg	gtg	gat	gga														
Met	Gln	Leu	Asn	Val	Thr	Gln	Gly	Thr	Val	Thr	Ile	Gly	Val	Asp	Gly														816
			260						265						270														
ttt	gcc	aca	gat	ggc	tta	cct	tat	ttg	gat	atc	att	gcc	aaa	aag	att														864
Phe	Ala	Thr	Asp	Gly	Leu	Pro	Tyr	Leu	Asp	Ile	Ile	Ala	Lys	Lys	Ile														
			275				280							285															
gaa	caa	aaa	caa	gcg	att	aca	aaa	gaa	aga	aca	gga	aat	tcc	gaa	acc														912
Glu	Gln	Lys	Gln	Ala	Ile	Thr	Lys	Glu	Arg	Thr	Gly	Asn	Ser	Glu	Thr														
			290				295						300																
gat	atc	act	ttt	gtc	gca	ggg	aac	agt	aaa	tat	gat	tta	aag	aca	cat														960
Asp	Ile	Thr	Phe	Val	Ala	Gly	Asn	Ser	Lys	Tyr	Asp	Leu	Lys	Thr	His														
			305			310					315				320														
caa	gtg	aca	gaa	aag	cat	acc	gct	gag	gca	caa	ggg	gaa	att	gcg	att														1008
Gln	Val	Thr	Glu	Lys	His	Thr	Ala	Glu	Ala	Gln	Gly	Glu	Ile	Ala	Ile														
				325				330						335															
agc	ggg	gcg	agt	acc	ggg	gca	atg	tac	ggg	aaa	aat	atc	aaa	tta	atc														1056
Ser	Gly	Ala	Ser	Thr	Gly	Ala	Met	Tyr	Gly	Lys	Asn	Ile	Lys	Leu	Ile														
			340					345						350															
gta	acg	gat	aaa	ggc	gct	ggg	gta	aaa	cat	gat	ggc	att	att	tta	tct														1104
Val	Thr	Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser														
			355				360						365																
gag	gcg	gat	att	caa	att	gaa	acc	cat	gag	ggc	gat	gtt	gaa	tta	ggc														1152
Glu	Ala	Asp	Ile	Gln	Ile	Glu	Thr	His	Glu	Gly	Asp	Val	Glu	Leu	Gly														
			370			375						380																	
aat	aca	aaa	aat	aat	cag	aat	gag	aat	tat	gcc	aaa	gct	cat	gcg	gaa														1200
Asn	Thr	Lys	Asn	Asn	Gln	Asn	Glu	Asn	Tyr	Ala	Lys	Ala	His	Ala	Glu														
			385			390				395				400															
ggg	aat	ttt	acg	gtt	aaa	ggc	ggg	aag	cac	gtt	att	att	ggg	aag	gaa														1248
Gly	Asn	Phe	Thr	Val	Lys	Gly	Gly	Lys	His	Val	Ile	Ile	Gly	Lys	Glu														
				405					410					415															
gtt	aaa	gcc	aac	aaa	gcg	gtc	gat	att	caa	gca	caa	gaa	aca	aca	gta														1296
Val	Lys	Ala	Asn	Lys	Ala	Val	Asp	Ile	Gln	Ala	Gln	Glu	Thr	Thr	Val														
				420				425					430																
aga	caa	aat	gcg	aaa	tta	act	gcc	aaa	acg	agt	gcc	aaa	att	aca	gca														1344
Arg	Gln	Asn	Ala	Lys	Leu	Thr	Ala	Lys	Thr	Ser	Ala	Lys	Ile	Thr	Ala														
			435				440					445																	
agt	aag	agt	gtg	aat	ctt	gaa	gat	aac	gcg	aaa	ctt	att	gct	aat	gag														1392
Ser	Lys	Ser	Val	Asn	Leu	Glu	Asp	Asn	Ala	Lys	Leu	Ile	Ala	Asn	Glu														
			450			455					460																		
ctg	agc	aca	aca	acc	aat	aaa	tta	acc	aat	aaa	ggg	agc	att	tac	ggc														1440
Leu	Ser	Thr	Thr	Thr	Asn	Lys	Leu	Thr	Asn	Lys	Gly	Ser	Ile	Tyr	Gly														
			465			470				475				480															
aag	aaa	gtg	acg	cta	gat	gct	gat	aat	tta	gtc	aat	agt	aaa	gaa	atc														1488
Lys	Lys	Val	Thr	Leu	Asp	Ala	Asp	Asn	Leu	Val	Asn	Ser	Lys	Glu	Ile														
				485				490						495															

tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu 500 505 510	1536
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser 515 520 525	1584
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly 530 535 540	1632
aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly 545 550 555 560	1680
aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn 565 570 575	1728
gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr 580 585 590	1776
atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala 595 600 605	1824
caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly 610 615 620	1872
ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly 625 630 635 640	1920
gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His 645 650 655	1968
tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu 660 665 670	2016
ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu 675 680 685	2064
att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys 690 695 700	2112
aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly 705 710 715 720	2160
tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser 725 730	2204

<210> 117

<211> 734  
 <212> PRT  
 <213> Pasteurella multocida

<400> 117  
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys  
 1 5 10 15  
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser  
 20 25 30  
 Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu  
 35 40 45  
 Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn  
 50 55 60  
 Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu  
 65 70 75 80  
 Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr  
 85 90 95  
 Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser  
 100 105 110  
 Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His  
 115 120 125  
 Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile  
 130 135 140  
 Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe  
 145 150 155 160  
 Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg  
 165 170 175  
 Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly  
 180 185 190  
 Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser  
 195 200 205  
 Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val  
 210 215 220  
 Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn  
 225 230 235 240  
 Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln  
 245 250 255  
 Met Gln Leu Asn Val Thr Gln Gly Thr Val Thr Ile Gly Val Asp Gly  
 260 265 270  
 Phe Ala Thr Asp Gly Leu Pro Tyr Leu Asp Ile Ile Ala Lys Lys Ile  
 275 280 285  
 Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr  
 290 295 300

Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His  
 305 310 315 320  
 Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile  
 325 330 335  
 Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile  
 340 345 350  
 Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser  
 355 360 365  
 Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly  
 370 375 380  
 Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu  
 385 390 395 400  
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu  
 405 410 415  
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val  
 420 425 430  
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala  
 435 440 445  
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu  
 450 455 460  
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly  
 465 470 475 480  
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile  
 485 490 495  
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu  
 500 505 510  
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser  
 515 520 525  
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly  
 530 535 540  
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly  
 545 550 555 560  
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn  
 565 570 575  
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr  
 580 585 590  
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala  
 595 600 605  
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly  
 610 615 620  
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly  
 625 630 635 640

Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His  
645 650 655

Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu  
660 665 670

Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu  
675 680 685

Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys  
690 695 700

Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly  
705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser  
725 730

<210> 118  
<211> 251  
<212> DNA  
<213> Pasteurella multocida

<220>  
<223> unkO

<220>  
<221> CDS  
<222> (1)..(249)

<400> 118  
atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48  
Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
1 5 10 15

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96  
Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
20 25 30

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144  
Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
35 40 45

gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192  
Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
50 55 60

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240  
Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
65 70 75 80

tgt aat cat ta 251  
Cys Asn His

<210> 119  
<211> 83  
<212> PRT  
<213> Pasteurella multocida  
  
<400> 119

Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser  
 1 5 10 15  
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala  
 20 25 30  
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly  
 35 40 45  
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly  
 50 55 60  
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His  
 65 70 75 80  
 Cys Asn His

<210> 120  
 <211> 548  
 <212> DNA  
 <213> Pasteurella multocida

<220>  
 <223> unkP

<220>  
 <221> CDS  
 <222> (1)..(546)

<400> 120  
 atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca 48  
 Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser  
 1 5 10 15  
 aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt 96  
 Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe  
 20 25 30  
 gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc 144  
 Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly  
 35 40 45  
 atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc 192  
 Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg  
 50 55 60  
 acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240  
 Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr  
 65 70 75 80  
 gca caa atc tta aaa gat acg att gca ggc gcg ttt gat tgg gca gtg 288  
 Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val  
 85 90 95  
 gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336  
 Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile  
 100 105 110  
 aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt 384  
 Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly

115                      120                      125  
 aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat    432  
 Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp  
     130                      135                      140  
  
 gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa    480  
 Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu  
     145                      150                      155                      160  
  
 cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt    528  
 Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe  
                                  165                      170                      175  
  
 tca aat cgt tta gca tcg ta                      548  
 Ser Asn Arg Leu Ala Ser  
                                  180  
  
 <210> 121  
 <211> 182  
 <212> PRT  
 <213> Pasteurella multocida  
  
 <400> 121  
 Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser  
     1                      5                      10                      15  
  
 Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe  
                                  20                      25                      30  
  
 Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly  
                                  35                      40                      45  
  
 Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg  
                                  50                      55                      60  
  
 Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr  
     65                      70                      75                      80  
  
 Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val  
                                  85                      90                      95  
  
 Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile  
                                  100                      105                      110  
  
 Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly  
                                  115                      120                      125  
  
 Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp  
                                  130                      135                      140  
  
 Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu  
     145                      150                      155                      160  
  
 Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe  
                                  165                      170                      175  
  
 Ser Asn Arg Leu Ala Ser  
                                  180

<210> 122  
 <211> 69  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvA-or1

<220>  
 <221> CDS  
 <222> (1)..(69)

<400> 122  
 atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48  
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
 1 5 10 15  
 gat aag ttt aag ata ctt agc 69  
 Asp Lys Phe Lys Ile Leu Ser  
 20

<210> 123  
 <211> 23  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 123  
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile  
 1 5 10 15  
 Asp Lys Phe Lys Ile Leu Ser  
 20

<210> 124  
 <211> 64  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvA-or2

<220>  
 <221> CDS  
 <222> (3)..(62)

<400> 124  
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta 47  
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu  
 1 5 10 15  
 ttg gca agc atg aca ta 64  
 Leu Ala Ser Met Thr  
 20

<210> 125  
 <211> 20  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 125

Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu  
1 5 10 15

Ala Ser Met Thr  
20

<210> 126

<211> 653

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvB

<220>

<221> CDS

<222> (1)..(651)

<400> 126

tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc 48  
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala  
1 5 10 15

gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa 96  
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys  
20 25 30

cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt 144  
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly  
35 40 45

aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa 192  
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu  
50 55 60

caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt 240  
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe  
65 70 75 80

gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt 288  
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser  
85 90 95

att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat 336  
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr  
100 105 110

aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa 384  
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu  
115 120 125

gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa 432  
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys  
130 135 140

tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca 480  
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser  
145 150 155 160

agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa 528

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln  
165 170 175

tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct 576  
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala  
180 185 190

tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat 624  
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn  
195 200 205

ctt ggc atg ggt tta tct gtc ggt tgg at 653  
Leu Gly Met Gly Leu Ser Val Gly Trp  
210 215

<210> 127  
<211> 217  
<212> PRT  
<213> Actinobacillus pleuropneumoniae

<400> 127  
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala  
1 5 10 15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys  
20 25 30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly  
35 40 45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu  
50 55 60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe  
65 70 75 80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser  
85 90 95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr  
100 105 110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu  
115 120 125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys  
130 135 140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser  
145 150 155 160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln  
165 170 175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala  
180 185 190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn  
195 200 205

Leu Gly Met Gly Leu Ser Val Gly Trp

&lt;210&gt; 128

&lt;211&gt; 242

&lt;212&gt; DNA

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;220&gt;

&lt;223&gt; apvC

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (240)

&lt;400&gt; 128

atg	tgg	cgg	atg	gga	gat	ttt	atg	tct	aaa	aaa	gag	agg	ctg	aat	gat	48
Met	Trp	Arg	Met	Gly	Asp	Phe	Met	Ser	Lys	Lys	Glu	Arg	Leu	Asn	Asp	
1				5					10					15		

atg	gct	cgc	cag	att	tta	tca	gcg	gcg	gag	ttg	ctc	att	gca	aag	gaa	96
Met	Ala	Arg	Gln	Ile	Leu	Ser	Ala	Ala	Glu	Leu	Leu	Ile	Ala	Lys	Glu	
			20					25					30			

ggc	ttg	caa	aat	tta	tcg	atg	agg	aaa	atc	gca	agt	gaa	gcc	ggc	atc	144
Gly	Leu	Gln	Asn	Leu	Ser	Met	Arg	Lys	Ile	Ala	Ser	Glu	Ala	Gly	Ile	
		35					40					45				

gca	aca	ggc	acg	ctt	tat	ctc	tat	ttc	aaa	acg	aaa	gac	gag	tta	ctg	192
Ala	Thr	Gly	Thr	Leu	Tyr	Leu	Tyr	Phe	Lys	Thr	Lys	Asp	Glu	Leu	Leu	
		50				55					60					

gat	tgt	ttg	gcg	gaa	caa	tta	cat	gaa	cga	tat	tat	cgt	tat	ctg	aat	240
Asp	Cys	Leu	Ala	Glu	Gln	Leu	His	Glu	Arg	Tyr	Tyr	Arg	Tyr	Leu	Asn	
65					70					75				80		

at																242
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&lt;210&gt; 129

&lt;211&gt; 80

&lt;212&gt; PRT

&lt;213&gt; Actinobacillus pleuropneumoniae

&lt;400&gt; 129

Met	Trp	Arg	Met	Gly	Asp	Phe	Met	Ser	Lys	Lys	Glu	Arg	Leu	Asn	Asp
1				5					10					15	

Met	Ala	Arg	Gln	Ile	Leu	Ser	Ala	Ala	Glu	Leu	Leu	Ile	Ala	Lys	Glu
			20					25					30		

Gly	Leu	Gln	Asn	Leu	Ser	Met	Arg	Lys	Ile	Ala	Ser	Glu	Ala	Gly	Ile
		35					40					45			

Ala	Thr	Gly	Thr	Leu	Tyr	Leu	Tyr	Phe	Lys	Thr	Lys	Asp	Glu	Leu	Leu
		50				55					60				

Asp	Cys	Leu	Ala	Glu	Gln	Leu	His	Glu	Arg	Tyr	Tyr	Arg	Tyr	Leu	Asn
65					70					75				80	

&lt;210&gt; 130

<211> 527  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> apvD

<220>  
 <221> CDS  
 <222> (1) .. (525)

<400> 130  
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 1 5 10 15  
 caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96  
 Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu  
 20 25 30  
 gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144  
 Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile  
 35 40 45  
 gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192  
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu  
 50 55 60  
 gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240  
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln  
 65 70 75 80  
 ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288  
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala  
 85 90 95  
 aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336  
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala  
 100 105 110  
 aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384  
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile  
 115 120 125  
 aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432  
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser  
 130 135 140  
 cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480  
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr  
 145 150 155 160  
 tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527  
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn  
 165 170 175

<210> 131  
 <211> 175  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 131  
 Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu  
 1 5 10 15  
 Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu  
 20 25 30  
 Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile  
 35 40 45  
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu  
 50 55 60  
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln  
 65 70 75 80  
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala  
 85 90 95  
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala  
 100 105 110  
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile  
 115 120 125  
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser  
 130 135 140  
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr  
 145 150 155 160  
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn  
 165 170 175

<210> 132  
 <211> 867  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> atpG

<220>  
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 <222> (1)..(864)

<400> 132  
 atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48  
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn  
 1 5 10 15  
 act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96  
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met  
 20 25 30  
 cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144  
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr  
 35 40 45  
 atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192  
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys

50	55	60	
cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240			
His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val 80			
65 70 75			
ggt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288			
Val Ser Thr Asp Arg Gly Leu Cys Gly Leu Asn Ile Asn Leu Phe 95			
85 90			
aaa cgc act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336			
Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Val Ser 110			
100 105			
ggt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384			
Val Gly Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn 125			
115 120			
cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432			
Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro 140			
130 135			
gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat cgc ttc 480			
Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe 160			
145 150 155			
cga aac gga gaa gtg gat cgc gtt tac gtc gct tac aac cgt ttt gaa 528			
Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu 175			
165 170			
aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576			
Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro 190			
180 185			
aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624			
Lys Leu Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile 205			
195 200			
tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672			
Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr 220			
210 215 220			
tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa 720			
Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu 240			
225 230 235			
caa gcc gct cga atg gta cgc atg aaa gcc gca aca gat aat cgc ggt 768			
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly 255			
245 250			
aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca 816			
Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala 270			
260 265 270			
agc att aca aat gaa tta aac gaa att gtt cgc ggt gcc gca gca att 864			
Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile 285			
275 280 285			
taa 867			

<210> 133

<211> 288  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 133

Met	Ala	Gly	Ala	Lys	Glu	Ile	Arg	Thr	Lys	Ile	Ala	Ser	Val	Lys	Asn
1				5					10					15	
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	20							25					30		
Arg	Lys	Thr	Gln	Glu	Arg	Met	Ala	Ala	Ser	Arg	Pro	Tyr	Ser	Glu	Thr
	35						40					45			
Ile	Arg	Lys	Val	Ile	Ser	His	Ile	Ala	Lys	Gly	Ser	Ile	Gly	Tyr	Lys
	50					55					60				
His	Pro	Phe	Leu	Thr	Glu	Arg	Asp	Ile	Lys	Lys	Val	Gly	Tyr	Leu	Val
	65				70					75				80	
Val	Ser	Thr	Asp	Arg	Gly	Leu	Cys	Gly	Gly	Leu	Asn	Ile	Asn	Leu	Phe
				85					90					95	
Lys	Ala	Thr	Leu	Asn	Glu	Phe	Lys	Thr	Trp	Lys	Asp	Lys	Asp	Val	Ser
	100							105						110	
Val	Glu	Leu	Gly	Leu	Val	Gly	Ser	Lys	Gly	Val	Ser	Phe	Tyr	Gln	Asn
	115						120						125		
Leu	Gly	Leu	Asn	Val	Arg	Ser	Gln	Val	Thr	Gly	Leu	Gly	Asp	Asn	Pro
	130					135					140				
Glu	Met	Glu	Arg	Ile	Val	Gly	Ala	Val	Asn	Glu	Met	Ile	Asn	Ala	Phe
	145				150					155				160	
Arg	Asn	Gly	Glu	Val	Asp	Ala	Val	Tyr	Val	Ala	Tyr	Asn	Arg	Phe	Glu
			165					170						175	
Asn	Thr	Met	Ser	Gln	Lys	Pro	Val	Ile	Ala	Gln	Leu	Leu	Pro	Leu	Pro
			180					185					190		
Lys	Leu	Asp	Asp	Asp	Glu	Leu	Asp	Thr	Lys	Gly	Ser	Trp	Asp	Tyr	Ile
	195						200					205			
Tyr	Glu	Pro	Asn	Pro	Gln	Val	Leu	Leu	Asp	Ser	Leu	Leu	Val	Arg	Tyr
	210					215					220				
Leu	Glu	Thr	Gln	Val	Tyr	Gln	Ala	Val	Val	Asp	Asn	Leu	Ala	Ser	Glu
	225				230					235				240	
Gln	Ala	Ala	Arg	Met	Val	Ala	Met	Lys	Ala	Ala	Thr	Asp	Asn	Ala	Gly
			245					250						255	
Thr	Leu	Ile	Asp	Glu	Leu	Gln	Leu	Val	Tyr	Asn	Lys	Ala	Arg	Gln	Ala
	260							265					270		
Ser	Ile	Thr	Asn	Glu	Leu	Asn	Glu	Ile	Val	Ala	Gly	Ala	Ala	Ala	Ile
	275						280					285			

<210> 134  
 <211> 534

<212> DNA  
<213> Actinobacillus pleuropneumoniae

<220>  
<223> atpH

<220>  
<221> CDS  
<222> (1)..(531)

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<400> 134
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1 5 10 15

gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
20 25 30

cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg cgc gaa tat att 144
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
35 40 45

aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192
Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
50 55 60

tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg 240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
65 70 75 80

gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc 288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
85 90 95

gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt 336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
100 105 110

tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg 384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
115 120 125

atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat 432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
130 135 140

aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att 480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
145 150 155 160

gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc 528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
165 170 175

ttg taa 534
Leu

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<210> 135  
<211> 177  
<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 135

Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe  
1 5 10 15

Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu  
20 25 30

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile  
35 40 45

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile  
50 55 60

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met  
65 70 75 80

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe  
85 90 95

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val  
100 105 110

Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala  
115 120 125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp  
130 135 140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile  
145 150 155 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser  
165 170 175

Leu

<210> 136

<211> 321

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dksA

<220>

<221> CDS

<222> (1) .. (318)

<400> 136

gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48  
Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln  
1 5 10 15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96  
Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr  
20 25 30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg  
35 40 45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192  
Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp  
50 55 60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240  
Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg  
65 70 75 80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288  
Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu  
85 90 95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321  
Ala Glu Ile Arg Glu Lys Gln Met Gly Leu  
100 105

<210> 137

<211> 106

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln  
1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr  
20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg  
35 40 45

Lys Leu Leu Lys Lys Ile Glu Thr Leu Asn Ser Ile Ala Glu Asp  
50 55 60

Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg  
65 70 75 80

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu  
85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu  
100 105

<210> 138

<211> 33

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dnaK

<220>

<221> CDS

<222> (1)..(30)

<400> 138

gct gag ttt gaa gaa gtg aaa gat aat aaa taa

33

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
1 5 10

<210> 139

<211> 10

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys  
1 5 10

<210> 140

<211> 453

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> exbB

<220>

<221> CDS

<222> (1) .. (450)

<400> 140

atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48  
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile  
1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96  
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile  
20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144  
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr  
35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192  
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser  
50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240  
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu  
65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288  
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile  
85 90 95

gac gcc gca tcc att atg gtt cac ctt tcg ctt gca tta aaa gca acc 336  
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr  
100 105 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384  
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly  
115 120 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432  
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln  
130 135 140

gct cgt aaa gcc aat caa taa  
Ala Arg Lys Ala Asn Gln  
145 150

<210> 141  
<211> 150  
<212> PRT  
<213> Actinobacillus pleuropneumoniae

<400> 141  
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile  
1 5 10 15  
Leu Gly Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile  
20 25 30  
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr  
35 40 45  
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser  
50 55 60  
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu  
65 70 75 80  
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile  
85 90 95  
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr  
100 105 110  
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly  
115 120 125  
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln  
130 135 140  
Ala Arg Lys Ala Asn Gln  
145 150

<210> 142  
<211> 720  
<212> DNA  
<213> Actinobacillus pleuropneumoniae

<220>  
<223> fkpA

<220>  
<221> CDS  
<222> (1) .. (717)

<400> 142  
atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48  
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
1 5 10 15  
gtt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat 96  
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
20 25 30

tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc 144  
 Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
 35 40 45

gtt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg 192  
 Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
 50 55 60

gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa 240  
 Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
 65 70 75 80

gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa 288  
 Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
 85 90 95

gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt 336  
 Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
 100 105 110

aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc 384  
 Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
 115 120 125

gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg 432  
 Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480  
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528  
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
 165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576  
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
 180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624  
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
 195 200 205

tac ggc gaa cgc caa gca ggt aag att ccg gca agt tca acc tta aaa 672  
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
 210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720  
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
 225 230 235

<210> 143  
 <211> 239  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 143  
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe  
 1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp  
                   20                                  25                                  30  
 Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val  
                   35                                  40                                  45  
 Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu  
                   50                                  55                                  60  
 Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu  
                   65                                  70                                  75                                  80  
 Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln  
                   85                                  90                                  95  
 Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly  
                   100                                  105                                  110  
 Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr  
                   115                                  120                                  125  
 Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser  
                   130                                  135                                  140  
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr  
                   145                                  150                                  155                                  160  
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu  
                   165                                  170                                  175  
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met  
                   180                                  185                                  190  
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly  
                   195                                  200                                  205  
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys  
                   210                                  215                                  220  
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys  
                   225                                  230                                  235

<210> 144

<211> 290

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> HI0379

<220>

<221> CDS

<222> (3) .. (287)

<400> 144

tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47  
   His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln  
       1                                  5                                  10                                  15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95  
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn

	20		25		30	
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct						143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser						
	35		40		45	
cag tgc tta acc cat tta tgg gaa cgt tta gaa gaa caa atc ggt						191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Gln Ile Gly						
	50		55		60	
gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg						239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser						
	65		70		75	
gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat						287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His						
	80		85		90	95
taa						290

<210> 145

<211> 95

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 145

His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro	
1 5 10 15	

Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu	
20 25 30	

Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln	
35 40 45	

Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val	
50 55 60	

Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp	
65 70 75 80	

His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His	
85 90 95	

<210> 146

<211> 273

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> hupA

<220>

<221> CDS

<222> (1)..(270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	

agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc 96  
 Ser Lys Lys Asp Ala Lys Ala Leu Glu Ala Thr Leu Asn Ala Ile  
           20                          25                          30  
 tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt 144  
 Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly  
           35                          40                          45  
 act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt 192  
 Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg  
           50                          55                          60  
 acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt 240  
 Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val  
           65                          70                          75                          80  
 gca ggt aaa gca tta aaa gat tta gta aaa taa 273  
 Ala Gly Lys Ala Leu Lys Asp Leu Val Lys  
                           85                          90

<210> 147

<211> 90

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu  
           1                          5                          10                          15

Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile  
           20                          25                          30

Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly  
           35                          40                          45

Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg  
           50                          55                          60

Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val  
           65                          70                          75                          80

Ala Gly Lys Ala Leu Lys Asp Leu Val Lys  
                           85                          90

<210> 148

<211> 551

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> lpda

<220>

<221> CDS

<222> (1) .. (549)

<400> 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct 48  
 Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro  
           1                          5                          10                          15

gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca 96  
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr  
20 25 30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144  
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val  
35 40 45

ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa 192  
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu  
50 55 60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240  
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn  
65 70 75 80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288  
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys  
85 90 95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336  
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val  
100 105 110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384  
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg  
115 120 125

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432  
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480  
Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528  
Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
165 170 175

gaa aaa att act cat tat ggg cc 551  
Glu Lys Ile Thr His Tyr Gly  
180

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro  
1 5 10 15

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr  
20 25 30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val  
35 40 45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu  
50 55 60

Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn  
 65 70 75 80  
 Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys  
 85 90 95  
 Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val  
 100 105 110  
 Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg  
 115 120 125  
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile  
 130 135 140  
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp  
 145 150 155 160  
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro  
 165 170 175  
 Glu Lys Ile Thr His Tyr Gly  
 180

<210> 150

<211> 1095

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1)..(1092)

<400> 150

atg aaa aaa tca tta gtt gct tta aca gta tta tgc gct gca gcg gta 48

Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Val 15

gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca 96

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala 30

ggt tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa 144

Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys 45

aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act 192

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr 50 55 60

tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt 240

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly 65 70 75 80

tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct 288

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser 85 90 95

gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca	336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala	
100 105 110	
cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac	384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp	
115 120 125	
tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat	432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr	
130 135 140	
aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa	480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln	
145 150 155 160	
agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa	528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Glu	
165 170 175	
tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca	576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala	
180 185 190	
agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat	624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp	
195 200 205	
atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg	672
Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala	
210 215 220	
gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc	720
Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser	
225 230 235 240	
tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg	768
Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala	
245 250 255	
gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta	816
Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu	
260 265 270	
tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa	864
Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys	
275 280 285	
gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct	912
Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala	
290 295 300	
aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta	960
Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val	
305 310 315 320	
ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt	1008
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val	
325 330 335	
aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt	1056
Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val	

340

345

350

gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa  
 Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met  
 355 360

1095

<210> 151  
 <211> 364  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 151  
 Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Val  
 1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala  
 20 25 30

Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys  
 35 40 45

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr  
 50 55 60

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly  
 65 70 75 80

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser  
 85 90 95

Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala  
 100 105 110

His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp  
 115 120 125

Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr  
 130 135 140

Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln  
 145 150 155 160

Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu  
 165 170 175

Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala  
 180 185 190

Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp  
 195 200 205

Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala  
 210 215 220

Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser  
 225 230 235 240

Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala  
 245 250 255

Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu

260                      265                      270  
 Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys  
           275                      280                      285  
 Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala  
           290                      295                      300  
 Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val  
           305                      310                      315                      320  
 Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val  
                                  325                      330                      335  
 Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val  
                                  340                      345                      350  
 Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met  
                                  355                      360

<210> 152  
 <211> 1110  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> Omp5

<220>  
 <221> CDS  
 <222> (1)..(1107)

<400> 152  
 atg aaa aaa tca tta gtt gct tta gca gta tta tca gct gca gca gta 48  
 Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Val  
           1                      5                      10                      15  
 gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt 96  
 Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val  
                                  20                      25                      30  
 ggt caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac 144  
 Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His  
                                  35                      40                      45  
 gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac 192  
 Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn  
                                  50                      55                      60  
 tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat 240  
 Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn  
                                  65                      70                      75                      80  
 aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta 288  
 Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val  
                                  85                      90                      95  
 cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt 336  
 Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly  
                                  100                      105                      110

tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac	384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp	
115 120 125	
gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa	432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys	
130 135 140	
tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta	480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu	
145 150 155 160	
aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct	528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro	
165 170 175	
gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac	576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn	
180 185 190	
tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa	624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln	
195 200 205	
tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc	672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe	
210 215 220	
ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa	720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys	
225 230 235 240	
aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc	768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser	
245 250 255	
tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc	816
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile	
260 265 270	
gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca	864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr	
275 280 285	
gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt	912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg	
290 295 300	
gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca	960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala	
305 310 315 320	
aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca	1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala	
325 330 335	
aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca	1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala	
340 345 350	
cgc gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct	1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala	

355

360

365

1110

atg taa  
Met

&lt;210&gt; 153

&lt;211&gt; 369

&lt;212&gt; PRT

<213> *Actinobacillus pleuropneumoniae*

&lt;400&gt; 153

Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Val  
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val  
20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His  
35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn  
50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn  
65 70 75 80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val  
85 90 95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly  
100 105 110

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp  
115 120 125

Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys  
130 135 140

Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu  
145 150 155 160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro  
165 170 175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn  
180 185 190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln  
195 200 205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe  
210 215 220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys  
225 230 235 240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser  
245 250 255

Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile  
260 265 270

Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr  
 275 280 285

Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg  
 290 295 300

Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala  
 305 310 315 320

Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala  
 325 330 335

Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala  
 340 345 350

Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala  
 355 360 365

Met

<210> 154  
 <211> 1076  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> pnp new

<220>  
 <221> CDS  
 <222> (1) .. (1074)

<400> 154  
 aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48  
 Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp  
 1 5 10 15

gtt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96  
 Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu  
 20 25 30

gcg gaa gcg cgt atc ggc gat gcg tat cgt att aca gaa aaa caa gcg 144  
 Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala  
 35 40 45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta 192  
 Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu  
 50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att 240  
 Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile  
 65 70 75 80

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc gcc gaa 288  
 Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu  
 85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336  
 Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile  
 100 105 110

tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg	384
115 120 125	
ggg gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp	432
130 135 140	
gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu	480
145 150 155 160	
ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile	528
165 170 175	
ggg tgc ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gcg aaa cgc Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg	576
180 185 190	
ggg gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val	624
195 200 205	
cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala	672
210 215 220	
tcg gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile	720
225 230 235 240	
aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu	768
245 250 255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly	816
260 265 270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu	864
275 280 285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile	912
290 295 300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met	960
305 310 315 320	
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro	1008
325 330 335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile	1056
340 345 350	
ggg aaa ggc ggt gcg gtt at Gly Lys Gly Gly Ala Val	1076

<210> 155  
 <211> 358  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 155

Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp  
 1 5 10 15  
 Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu  
 20 25 30  
 Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala  
 35 40 45  
 Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu  
 50 55 60  
 Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile  
 65 70 75 80  
 Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu  
 85 90 95  
 Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile  
 100 105 110  
 Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg  
 115 120 125  
 Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp  
 130 135 140  
 Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu  
 145 150 155 160  
 Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile  
 165 170 175  
 Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg  
 180 185 190  
 Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val  
 195 200 205  
 Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala  
 210 215 220  
 Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile  
 225 230 235 240  
 Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu  
 245 250 255  
 Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly  
 260 265 270  
 Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu  
 275 280 285

Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile  
290 295 300

Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met  
305 310 315 320

Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro  
325 330 335

Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile  
340 345 350

Gly Lys Gly Gly Ala Val  
355

<210> 156

<211> 1055

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> potD

<220>

<221> CDS

<222> (1) .. (1053)

<400> 156

atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca 48  
Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala  
1 5 10 15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96  
Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala  
20 25 30

caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat 144  
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr  
35 40 45

gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa 192  
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys  
50 55 60

gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta 240  
Val Glu Val Ser Ser Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu  
65 70 75 80

aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac 288  
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn  
85 90 95

tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat 336  
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp  
100 105 110

cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac 384  
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn  
115 120 125

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt 432

Lys	Pro	Tyr	Asp	Gln	Gly	Asn	Lys	Tyr	Ser	Leu	Pro	Gln	Leu	Leu	Gly	
130						135					140					
gca	ccg	ggg	atc	gca	ttt	aac	tca	aat	gac	tat	aag	ggc	gat	gcg	ttc	480
Ala	Pro	Gly	Ile	Ala	Phe	Asn	Ser	Asn	Asp	Tyr	Lys	Gly	Asp	Ala	Phe	
145					150					155					160	
act	tct	tg	ggg	gat	tta	tg	aaa	cct	gag	ttt	gcg	aat	aaa	gta	caa	528
Thr	Ser	Trp	Gly	Asp	Leu	Trp	Lys	Pro	Glu	Phe	Ala	Asn	Lys	Val	Gln	
				165					170					175		
tta	tta	gat	gac	gca	cgt	gaa	gta	ttt	aac	att	gcg	tta	tta	aaa	tta	576
Leu	Leu	Asp	Asp	Ala	Arg	Glu	Val	Phe	Asn	Ile	Ala	Leu	Leu	Lys	Leu	
				180				185					190			
ggg	aaa	aac	cct	aat	aca	acc	aat	ccg	gaa	gag	att	aaa	gcg	gct	tac	624
Gly	Lys	Asn	Pro	Asn	Thr	Thr	Asn	Pro	Glu	Glu	Ile	Lys	Ala	Ala	Tyr	
		195					200				205					
gaa	gag	tta	aga	aaa	tta	cgt	cca	aac	gta	ctt	tct	ttc	act	tca	gac	672
Glu	Glu	Leu	Arg	Lys	Leu	Arg	Pro	Asn	Val	Leu	Ser	Phe	Thr	Ser	Asp	
		210				215					220					
aac	cca	gcg	aac	tca	ttt	atc	gca	ggg	gaa	gta	tct	gta	ggg	caa	tta	720
Asn	Pro	Ala	Asn	Ser	Phe	Ile	Ala	Gly	Glu	Val	Ser	Val	Gly	Gln	Leu	
225				230				235							240	
tg	aac	ggg	tct	gta	cgt	att	gcg	aaa	aaa	gaa	caa	gcg	ccg	gta	aac	768
Trp	Asn	Gly	Ser	Val	Arg	Ile	Ala	Lys	Lys	Glu	Gln	Ala	Pro	Val	Asn	
				245				250						255		
atg	gtg	ttc	cca	aaa	gaa	ggg	cct	gta	ctt	tg	gtt	gat	acg	tta	gcc	816
Met	Val	Phe	Pro	Lys	Glu	Gly	Pro	Val	Leu	Trp	Val	Asp	Thr	Leu	Ala	
			260					265					270			
att	ccg	gcg	aat	gcg	aaa	aac	aaa	gaa	aat	gcg	cat	aag	tta	atc	aac	864
Ile	Pro	Ala	Asn	Ala	Lys	Asn	Lys	Glu	Asn	Ala	His	Lys	Leu	Ile	Asn	
		275				280						285				
tac	tta	tta	agc	gca	ccg	gtt	gcg	gaa	aaa	tta	acg	tta	gaa	atc	ggg	912
Tyr	Leu	Leu	Ser	Ala	Pro	Val	Ala	Glu	Lys	Leu	Thr	Leu	Glu	Ile	Gly	
		290				295					300					
tat	ccg	act	tca	aac	gta	gaa	gcg	tta	aaa	aca	tta	cca	aaa	gag	att	960
Tyr	Pro	Thr	Ser	Asn	Val	Glu	Ala	Leu	Lys	Thr	Leu	Pro	Lys	Glu	Ile	
305					310					315				320		
acc	gaa	gat	ccg	gca	atc	tat	ccg	aca	gct	gat	gtg	tta	aaa	gcg	gca	1008
Thr	Glu	Asp	Pro	Ala	Ile	Tyr	Pro	Thr	Ala	Asp	Val	Leu	Lys	Ala	Ala	
				325					330					335		
caa	tg	caa	gac	gat	gta	ggg	aat	gca	atc	gaa	ctt	tac	gaa	aaa	ta	1055
Gln	Trp	Gln	Asp	Asp	Val	Gly	Asn	Ala	Ile	Glu	Leu	Tyr	Glu	Lys		
		340					345						350			

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala  
1 5 10 15

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala  
20 25 30

Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr  
35 40 45

Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys  
50 55 60

Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu  
65 70 75 80

Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn  
85 90 95

Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp  
100 105 110

His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn  
115 120 125

Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly  
130 135 140

Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe  
145 150 155 160

Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln  
165 170 175

Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu  
180 185 190

Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr  
195 200 205

Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp  
210 215 220

Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu  
225 230 235 240

Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn  
245 250 255

Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala  
260 265 270

Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn  
275 280 285

Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly  
290 295 300

Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile  
305 310 315 320

Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala  
325 330 335

Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys  
 340 345 350

<210> 158  
 <211> 525  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> rpmF

<220>  
 <221> CDS  
 <222> (1)..(522)

<400> 158  
 atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct 48  
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala  
 1 5 10  
 cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96  
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn  
 20 25 30  
 cgt ttg ggt gaa tct gtg agc aat gtg cta agc gat gca caa gtt act 144  
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr  
 35 40 45  
 ctc tgc tta tat atc gat ccg caa cgc tta acc gtt att aaa ggt acg 192  
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr  
 50 55 60  
 gcg aca gtg gaa gtg gaa ttc gat tgc caa cga tgc ggt aac ccg ttt 240  
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
 65 70 75 80  
 aca caa acg ctt gac tgt tgc ttt tgt ttc agt ccg gtg tcc aat atg 288  
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
 85 90 95  
 gat cag cgc gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336  
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
 100 105 110  
 gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384  
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
 115 120 125  
 atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432  
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
 130 135 140  
 tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480  
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
 145 150 155 160  
 aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525  
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
 165 170

<210> 159  
 <211> 174  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 159  
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala  
 1 5 10 15  
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn  
 20 25 30  
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr  
 35 40 45  
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr  
 50 55 60  
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe  
 65 70 75 80  
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met  
 85 90 95  
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn  
 100 105 110  
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile  
 115 120 125  
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val  
 130 135 140  
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys  
 145 150 155 160  
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn  
 165 170

<210> 160  
 <211> 1302  
 <212> DNA  
 <213> Actinobacillus pleuropneumoniae

<220>  
 <223> tig

<220>  
 <221> CDS  
 <222> (1) .. (1299)

<400> 160  
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48  
 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr  
 1 5 10 15  
 att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96  
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu  
 20 25 30  
 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys	
35 40 45	
gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa	192
Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln	
50 55 60	
gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc	240
Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile	
65 70 75 80	
gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac	288
Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn	
85 90 95	
tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc	336
Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe	
100 105 110	
ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg	384
Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro	
115 120 125	
gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta	432
Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu	
130 135 140	
cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg	480
Arg Lys Gln Gln Ala Thr Tip Ala Glu Ser Gln Ala Ala Ala Gln Ala	
145 150 155 160	
gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag	528
Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu	
165 170 175	
ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt	576
Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser	
180 185 190	
cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc gcc	624
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly	
195 200 205	
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa	672
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu	
210 215 220	
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta	720
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val	
225 230 235 240	
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc	768
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe	
245 250 255	
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat	816
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn	
260 265 270	
atg caa cgt gaa ctt aaa aac gca gta acc gca gcg gtt aaa aac caa	864
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln	
275 280 285	

gta atc aac ggt tta atc gca caa aat gaa att gaa gtg cgg gct gca 912  
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala  
290 295 300

gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt 960  
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg  
305 310 315 320

ttc ggt ggt aaa cgg gaa atg gct gca caa tta cgg gcg gaa tta ttc 1008  
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe  
325 330 335

gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc 1056  
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Ser Thr  
340 345 350

gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa 1104  
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu  
355 360 365

acg att gca gaa atc gct tca gct tac gaa caa cgg gcg gaa gtt gtt 1152  
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val  
370 375 380

gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta 1200  
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val  
385 390 395 400

gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta 1248  
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val  
405 410 415

act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa 1296  
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln  
420 425 430

ggc taa 1302  
Gly

<210> 161  
<211> 433  
<212> PRT  
<213> Actinobacillus pleuropneumoniae

<400> 161  
Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr  
1 5 10 15  
Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu  
20 25 30  
Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys  
35 40 45  
Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln  
50 55 60  
Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Asp Ala Val Ile  
65 70 75 80  
Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe  
 100 105  
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro  
 115 120 125  
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu  
 130 135 140  
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala  
 145 150 155 160  
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu  
 165 170 175  
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser  
 180 185 190  
 Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly  
 195 200 205  
 Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu  
 210 215 220  
 Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val  
 225 230 235 240  
 Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe  
 245 250 255  
 Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn  
 260 265 270  
 Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln  
 275 280 285  
 Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala  
 290 295 300  
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg  
 305 310 315 320  
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe  
 325 330 335  
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr  
 340 345 350  
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu  
 355 360 365  
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val  
 370 375 380  
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val  
 385 390 395 400  
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val  
 405 410 415

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln  
420 425 430

Gly

<210> 162  
<211> 316  
<212> DNA  
<213> Actinobacillus pleuropneumoniae

<220>  
<223> tRNA-glu

<400> 162  
aatattgcgc tcaaatggca aagcggagag catctttaa tgtgtcccc atcgtctaga 60  
ggcctaggac atcgcccttt cacggcggtt accgggggtc gaatccccgt ggggacgcc 120  
tttaagatg acttttgttg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180  
tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatcct 240  
agctgaacaa aagcagctaa gtgttagtt gaataaagta tcgcgttgaa tgcgttcaaa 300  
taaaatttga aaatat 316

<210> 163  
<211> 85  
<212> DNA  
<213> Actinobacillus pleuropneumoniae

<220>  
<223> tRNA-leu

<400> 163  
gctctggttg tggaattggt agacacgcta tcttgagggg gtagtgcca taggatgtgc 60  
gagttcgagt ctcgccaga gcacc 85

<210> 164  
<211> 623  
<212> DNA  
<213> Actinobacillus pleuropneumoniae

<220>  
<223> yaeE

<220>  
<221> CDS  
<222> (1) .. (621)

<400> 164  
atg caa gaa ctc aca cct caa atg tgg ggc tta gtc ggc act tca acg 48  
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr  
1 5 10 15  
ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta 96  
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val

20	25	30	
gtc ggt ttg ccg atc ggt ttt	ctg gca ttt tta acc ggt aaa gga gag	144	
Val Gly Leu Pro Ile Gly Phe	Leu Ala Phe Leu Thr Gly Lys Gly Glu		
35	40	45	
att tta gag aat ccg cgt tta cat caa gta tta gat	gtg att att aat	192	
Ile Leu Glu Asn Pro Arg Leu His	Gln Val Leu Asp Val Ile Ile Asn		
50	55	60	
atc ggt cgt tcc gta ccg ttt att att ttg tta gtc	gtg ttg tta cct	240	
Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val	Val Val Leu Leu Pro		
65	70	75	80
ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act	acg gcg gcg att	288	
Phe Thr Arg Leu Leu Val Gly Thr Thr	Leu Gly Thr Thr Ala Ala Ile		
85	90	95	
gtg ccg tta agc gtt tgc gca att ccg ttt ttt gcg	cgt tta act tca	336	
Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala	Arg Leu Thr Ser		
100	105	110	
aat gcg tta tta gaa atc cca gca ggt tta acc gaa	gcg gcg aaa tgc	384	
Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr	Glu Ala Ala Lys Ser		
115	120	125	
atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt	tat tta ccg gaa	432	
Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys	Phe Tyr Leu Pro Glu		
130	135	140	
tca ctg ccg att tta atc aat ggt atc aca tta act	tta gtc gct tta	480	
Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr	Leu Val Ala Leu		
145	150	155	160
atc ggt tat tgc gca atg gcg ggt gcg gtc ggc ggc	ggc ggt ttg ggt	528	
Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly	Gly Gly Leu Gly		
165	170	175	
aac ctt gcc atc agt tac ggt gaa cac cga aat atg	gtc tat gta aaa	576	
Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met	Val Tyr Val Lys		
180	185	190	
tgg atc tca aca att att atc gta gcg att gtg atg	atc agt caa aa	623	
Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met	Ile Ser Gln		
195	200	205	

<210> 165  
 <211> 207  
 <212> PRT  
 <213> Actinobacillus pleuropneumoniae

<400> 165  
 Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr  
 1 5 10 15  
 Leu Glu Thr Leu Tyr Met Gly Phe Ala Thr Leu Leu Ala Val Val  
 20 25 30  
 Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu  
 35 40 45

Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn  
 50 55 60  
 Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro  
 65 70 75 80  
 Phe Thr Arg Leu Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile  
 85 90 95  
 Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser  
 100 105 110  
 Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser  
 115 120 125  
 Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu  
 130 135 140  
 Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu  
 145 150 155 160  
 Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly  
 165 170 175  
 Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys  
 180 185 190  
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln  
 195 200 205